66-

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images, please do not report the images to the Image Problem Mailbox.

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 17:10:34 ; Search time 1444.83 Seconds
(without alignments)
224.186 Million cell updates/sec

Title: US-09-719-737-2
Perfect score: 20
Sequence: 1 gttcccagagcttgccacct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	13.6	68.0	36	17	AL752038	AL752038 Arabidops
	2	13.6	68.0	43	17	BH811442	BH811442 SALK_0586
c	3	12.6	63.0	46	12	BF983620	BF983620 602304738
c	4	12.4	62.0	40	12	BF784339	BF784339 602110114
	5	12.2	61.0	31	17	AZ435998	AZ435998 1M0223N19
	6	12.2	61.0	40	9	AI708971	AI708971 as61d12.x
	7	12.2	61.0	46	9	AA576353	AA576353 nh10g03.s
	8	12	60.0	50	9	AU103972	AU103972 AU103972
	9	12	60.0	50	9	AU106874	AU106874 AU106874
	10	12	60.0	50	9	AU106878	AU106878 AU106878
c	11	11.8	59.0	21	17	AZ647787	AZ647787 1M0514P24
	12	11.8	59.0	44	14	H44436	H44436 yo75b02.s1
	13	11.6	58.0	27	17	AZ387826	AZ387826 1M0147E22
	14	11.6	58.0	29	17	AZ310013	AZ310013 1M0018B12
	15	11.6	58.0	37	17	AZ338635	AZ338635 1M0069I15
c	16	11.6	58.0	44	17	AZ502054	AZ502054 1M0341I10
c	17	11.6	58.0	45	17	AZ760255	AZ760255 1M0553F22
	18	11.6	58.0	50	9	AU103964	AU103964 AU103964
	19	11.6	58.0	50	9	AU103967	AU103967 AU103967
c	20	11.6	58.0	50	9	AU105804	AU105804 AU105804
c	21	11.6	58.0	50	9	AU107143	AU107143 AU107143
c	22	11.6	58.0	50	9	AU107145	AU107145 AU107145
c	23	11.6	58.0	50	9	AU107146	AU107146 AU107146
c	24	11.4	57.0	46	17	AZ768227	AZ768227 1M0568C08
c	25	11.4	57.0	50	9	AU102274	AU102274 AU102274
	26	11.4	57.0	50	9	AU102757	AU102757 AU102757
	27	11.2	56.0	27	17	AZ655087	AZ655087 1M0529C23
	28	11.2	56.0	36	13	BG973952	BG973952 602843604
	29	11.2	56.0	37	9	AI647510	AI647510 uk40e11.x
	30	11.2	56.0	39	13	BI078535	BI078535 602872804
c	31	11.2	56.0	40	17	AZ378558	AZ378558 1M0133E23
	32	11.2	56.0	42	14	H14364	H14364 ym18e07.s1
c	33	11.2	56.0	42	17	BH626517	BH626517 1007110D0
c	34	11.2	56.0	43	9	AA994992	AA994992 ou09b09.s
c	35	11.2	56.0	43	14	R79446	R79446 yi87f11.s1
c	36	11.2	56.0	44	10	AV844185	AV844185 AV844185
	37	11.2	56.0	46	12	BF533864	BF533864 602075209
	38	11.2	56.0	48	12	BF232745	BF232745 602023341
	39	11.2	56.0	48	12	BF235094	BF235094 602027858
c	40	11.2	56.0	48	17	AZ800533	AZ800533 2M0058A12
c	41	11.2	56.0	49	9	AI560790	AI560790 tn22d06.x
	42	11.2	56.0	49	9	AA572078	AA572078 vk95f07.r
c	43	11.2	56.0	50	9	AU102678	AU102678 AU102678
	44	11.2	56.0	50	9	AU104734	AU104734 AU104734
c	45	11.2	56.0	50	9	AU105732	AU105732 AU105732

ALIGNMENTS

RESULT 1
AL752038/c
LOCUS AL752038 36 bp DNA linear GSS 17-JUN-2002
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-010E07-014869, genomic survey sequence.
ACCESSION AL752038
VERSION AL752038.1 GI:21484536
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H. and Weisshaar,B.
TITLE A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
JOURNAL Unpublished
REFERENCE 2
AUTHORS Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 36)
AUTHORS Rosso,M., Li,Y., Strizhov,N. and Weisshaar,B.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer

```
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion within the locus defined by clone t5m2. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-010E07-014869"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC106. The lines contain one or more T-DNA
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thalaina nuclear genome sequence were
                     processed for submission. T-DNA derived sequences were
                     removed"
BASE COUNT        7 a      8 c      11 g      10 t
ORIGIN

  Query Match             68.0%;  Score 13.6;  DB 17;  Length 36;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCCACCT 20
           | ||||| ||| ||||| ||
Db      34 GATCCCATAGCCTGCCAGCT 15


RESULT 2
BH811442
LOCUS       BH811442                  43 bp    DNA     linear   GSS 02-MAY-2002
DEFINITION  SALK_058616 Arabidopsis thaliana TDNA insertion lines Arabidopsis
            thallana genomic clone SALK_058616, DNA sequence.
ACCESSION   BH811442
VERSION     BH811442.1  GI:20389897
KEYWORDS    GSS.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_058616"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains one or more TDNA insertion
                     elements. The resultant fragment for each line was
                     directly sequenced to determine the genomic sequence at
                     the site of insertion. Details of the protocols used can
                     be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT        8 a      13 c      7 g      15 t
ORIGIN

  Query Match             68.0%;  Score 13.6;  DB 17;  Length 43;
  Best Local Similarity   80.0%;  Pred. No. 2.1e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCCACCT 20
           | ||||| ||| |||| |||
Db      14 GGTCCCAAAGCCTGCCGCCT 33


RESULT 3
BF983620/c
LOCUS       BF983620                  46 bp    mRNA    linear   EST 23-JAN-2001
DEFINITION  602304738F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4396185 5',
            mRNA sequence.
ACCESSION   BF983620
VERSION     BF983620.1  GI:12386432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10094  row: l  column: 10
            High quality sequence stop: 46.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4396185"
                     /clone_lib="NIH_MGC_88"
                     /tissue_type="duodenal adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: small intestine; Vector: pCMV-SPORT6;
                     Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
                     oligo-dT primed. Average insert size 1.767 kb. Library
                     enriched for full-length clones and constructed by Life
                     Technologies. Note: this is a NIH_MGC Library."
BASE COUNT        7 a      16 c      15 g      8 t
ORIGIN

  Query Match             63.0%;  Score 12.6;  DB 12;  Length 46;
  Best Local Similarity   78.9%;  Pred. No. 6.1e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCCACC 19
           | || || |||||||| ||
Db      38 GGTCGCACAGCTTGCCGCC 20


RESULT 4
BF784339/c
LOCUS       BF784339                  40 bp    mRNA    linear   EST 12-JAN-2001
```

```
DEFINITION  602110114F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4238354
            5', mRNA sequence.
ACCESSION   BF784339
VERSION     BF784339.1  GI:12089375
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9849  row: 1  column: 03
            High quality sequence stop: 39.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4238354"
                     /clone_lib="NCI_CGAP_Kid14"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT        2 a     11 c     17 g     10 t
ORIGIN

  Query Match             62.0%;  Score 12.4;  DB 12;  Length 40;
  Best Local Similarity   92.9%;  Pred. No. 7.1e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      6 CAGAGCTTGCCACC 19
          |||||||| |||||
Db     24 CAGAGCTTCCCACC 11


RESULT 5
AZ435998
LOCUS       AZ435998                 31 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0223N19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0223N19 F, DNA sequence.
ACCESSION   AZ435998
VERSION     AZ435998.1  GI:10560011
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0223  row: N  column: 19
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 31.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0223N19"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        5 a     12 c      6 g      8 t
ORIGIN

  Query Match             61.0%;  Score 12.2;  DB 17;  Length 31;
  Best Local Similarity   82.4%;  Pred. No. 8e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      4 CCCAGAGCTTGCCACCT 20
            ||| |||  ||||||||
Db      2 CCCTGAGGCTGCCACCT 18


RESULT 6
AI708971
LOCUS       AI708971                 40 bp    mRNA    linear   EST 04-JUN-1999
DEFINITION  as61d12.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone
            IMAGE:2333207 3' similar to SW:RL10_HUMAN P27635 60S RIBOSOMAL
            PROTEIN L10 ;, mRNA sequence.
ACCESSION   AI708971
VERSION     AI708971.1  GI:4998747
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
            ,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
```

```
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2333207"
                     /clone_lib="Barstead colon HPLRB7"
                     /sex="male"
                     /dev_stage="adult, age 25"
                     /lab_host="DH10B (phage resistant)"
                     /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACGAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     [5' AATTCACTAGTAAT 3' and 5' ATTACTAGTG 3'], digested
                     with Not I and cloned into the Not I and Eco RI sites of
                     the modified pT7T3 vector. Library constructed by Bob
                     Barstead."
BASE COUNT        9 a      9 c     10 g     12 t
ORIGIN

  Query Match             61.0%;  Score 12.2;  DB 9;  Length 40;
  Best Local Similarity   82.4%;  Pred. No. 8.8e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3 TCCCAGAGCTTGCCACC 19
           |||||||||  | ||||
Db      19 TCCCAGAGCAAGACACC 35


RESULT 7
AA576353
LOCUS       AA576353                 46 bp    mRNA    linear   EST 04-SEP-1997
DEFINITION  nh10g03.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951988 3'
            similar to SW:RL3_HUMAN P39023 60S RIBOSOMAL PROTEIN L3. ;, mRNA
            sequence.
ACCESSION   AA576353
VERSION     AA576353.1  GI:2353827
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies Inc., David Krizman,
            Ph.D.
             cDNA Library Arraying: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 1392   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:951988"
                     /clone_lib="NCI_CGAP_Co1"
                     /tissue_type="bulk tumor"
                     /lab_host="DH10B"
                     /note="Organ: colon; Vector: pCMV-SPORT2; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT."
BASE COUNT       12 a     13 c     14 g      7 t
ORIGIN

  Query Match             61.0%;  Score 12.2;  DB 9;  Length 46;
  Best Local Similarity   82.4%;  Pred. No. 9.3e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 TTCCCAGAGCTTGCCAC 18
           || |||| || ||||||
Db       6 TTGCCAGCGCGTGCCAC 22


RESULT 8
AU103972
LOCUS       AU103972                 50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU103972 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            KAT06150, mRNA sequence.
ACCESSION   AU103972
VERSION     AU103972.1  GI:13553493
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="KAT06150"
                     /clone_lib="Sugano Homo sapiens cDNA library"
                     /note="Differential display comparison of untreated and
                     dimethylfumarate treated U937 cells"
BASE COUNT        8 a     12 c     21 g      9 t
ORIGIN

  Query Match             60.0%;  Score 12;  DB 9;  Length 50;
  Best Local Similarity   75.0%;  Pred. No. 1.2e+05;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCCACCT 20
           ||||||||||   | ||| |
Db       8 GTTCCCAGAGTGGGGCACAT 27


RESULT 9
AU106874
LOCUS       AU106874                 50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU106874 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            KAT01514, mRNA sequence.
```

```
ACCESSION   AU106874
VERSION     AU106874.1  GI:13556395
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="KAT01514"
                     /clone_lib="Sugano Homo sapiens cDNA library"
                     /note="Differential display comparison of untreated and
                     dimethylfumarate treated U937 cells"
BASE COUNT        3 a     15 c     22 g     10 t
ORIGIN

  Query Match             60.0%;  Score 12;  DB 9;  Length 50;
  Best Local Similarity   75.0%;  Pred. No. 1.2e+05;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCCACCT 20
           || ||| ||  ||||| |||
Db      30 GTGCCCCGACGTTGCCCCCT 49


RESULT 10
AU106878
LOCUS       AU106878                 50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU106878 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            KAT09217, mRNA sequence.
ACCESSION   AU106878
VERSION     AU106878.1  GI:13556399
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="KAT09217"
                     /clone_lib="Sugano Homo sapiens cDNA library"
                     /note="Differential display comparison of untreated and
                     dimethylfumarate treated U937 cells"
BASE COUNT        4 a     16 c     21 g      9 t
ORIGIN

  Query Match             60.0%;  Score 12;  DB 9;  Length 50;
  Best Local Similarity   75.0%;  Pred. No. 1.2e+05;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCCACCT 20
           || ||| ||  ||||| |||
Db      29 GTGCCCCGACTTTGCCCCCT 48


RESULT 11
AZ647787/c
LOCUS       AZ647787                 21 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0514P24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0514P24 F, DNA sequence.
ACCESSION   AZ647787
VERSION     AZ647787.1  GI:11779601
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000  Std Error: 0.00
            Plate: 0514  row: P  column: 24
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0514P24"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
```

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 2 a 4 c 9 g 6 t
ORIGIN

Query Match 59.0%; Score 11.8; DB 17; Length 21;
Best Local Similarity 86.7%; Pred. No. 1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCCCAGAGCTTGCCA 17
||||| ||| |||||
Db 15 TCCCACAGCATGCCA 1

RESULT 12
H44436
LOCUS H44436 44 bp mRNA linear EST 31-JUL-1995
DEFINITION yo75b02.s1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:183723 3' similar to gb:M63167 RAC-ALPHA SERINE/THREONINE KINASE (HUMAN);, mRNA sequence.
ACCESSION H44436
VERSION H44436.1 GI:920488
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 44)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 643
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 643 Std Error: 0.00
Seq primer: Promega -21m13
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .44
/organism="Homo sapiens"
/db_xref="GDB:3816923"
/db_xref="taxon:9606"
/clone="IMAGE:183723"
/clone_lib="Soares breast 3NbHBst"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: breast; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 4 a 15 c 20 g 2 t 3 others
ORIGIN

Query Match 59.0%; Score 11.8; DB 14; Length 44;
Best Local Similarity 81.2%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CCCAGAGCTTGCCACC 19
||||| | | ||||||
Db 20 CCCAGGGNTGGCCACC 35

RESULT 13
AZ387826
LOCUS AZ387826 27 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0147E22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0147E22 R, DNA sequence.
ACCESSION AZ387826
VERSION AZ387826.1 GI:10501534
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0147 row: E column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
FEATURES Location/Qualifiers
source 1. .27
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0147E22"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."
BASE COUNT 6 a 9 c 3 g 9 t
ORIGIN

Query Match 58.0%; Score 11.6; DB 17; Length 27;
Best Local Similarity 77.8%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy      2 TTCCCAGAGCTTGCCACC 19
          ||||||  ||  | |||||
Db      1 TTCCCATAGGCTCCCACC 18
```

RESULT 14
AZ310013
LOCUS AZ310013 29 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0018B12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0018B12 R, DNA sequence.
ACCESSION AZ310013
VERSION AZ310013.1 GI:10351576
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: B column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.
FEATURES Location/Qualifiers
source 1. .29
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0018B12"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."
BASE COUNT 0 a 14 c 6 g 9 t
ORIGIN

Query Match 58.0%; Score 11.6; DB 17; Length 29;
Best Local Similarity 77.8%; Pred. No. 1.5e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy      3 TCCCAGAGCTTGCCACCT 20
          |||| | |||||||  ||
Db      4 TCCCCGTGCTTGCCTGCT 21
```

RESULT 15
AZ338635
LOCUS AZ338635 37 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0069I15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0069I15 R, DNA sequence.
ACCESSION AZ338635
VERSION AZ338635.1 GI:10412103
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 37)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0069 row: I column: 15
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 37.
FEATURES Location/Qualifiers
source 1. .37
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0069I15"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."
BASE COUNT 14 a 11 c 7 g 5 t
ORIGIN

Query Match 58.0%; Score 11.6; DB 17; Length 37;
Best Local Similarity 77.8%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       1 GTTCCCAGAGCTTGCCAC 18
           || | || |||| |||||
Db       6 GTCCTCAAAGCTGGCCAC 23
```

Search completed: November 28, 2002, 19:30:41
Job time : 1447.83 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 17:15:39 ; Search time 42.069 Seconds
(without alignments)
183.088 Million cell updates/sec

Title: US-09-719-737-2
Perfect score: 20
Sequence: 1 gttcccagagcttgccacct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 341543 seqs, 192557720 residues

Total number of hits satisfying chosen parameters: 177872

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	14.4	72.0	20	10	US-09-752-639-36	Sequence 36, Appl
	2	14.4	72.0	20	10	US-09-984-198-36	Sequence 36, Appl
	3	13.6	68.0	25	10	US-09-815-153-9	Sequence 9, Appli
	4	13.2	66.0	31	10	US-09-801-274-992	Sequence 992, App
	5	12.6	63.0	20	10	US-09-841-366A-33	Sequence 33, Appl
	6	12.4	62.0	19	10	US-09-216-393-289	Sequence 289, App
c	7	12.2	61.0	20	9	US-09-944-413-99	Sequence 99, Appl
c	8	12.2	61.0	20	9	US-09-944-403-99	Sequence 99, Appl
c	9	12.2	61.0	20	9	US-09-944-896-99	Sequence 99, Appl
c	10	12.2	61.0	20	9	US-09-944-944-99	Sequence 99, Appl
c	11	12.2	61.0	20	10	US-09-866-028-99	Sequence 99, Appl
c	12	12.2	61.0	20	10	US-09-944-449-99	Sequence 99, Appl
c	13	12.2	61.0	20	10	US-09-944-457-99	Sequence 99, Appl
c	14	12.2	61.0	20	10	US-09-945-587-99	Sequence 99, Appl
c	15	12.2	61.0	20	10	US-09-945-015-99	Sequence 99, Appl
c	16	12.2	61.0	20	10	US-09-944-396-99	Sequence 99, Appl
c	17	12.2	61.0	20	10	US-09-944-097-99	Sequence 99, Appl
c	18	12.2	61.0	20	10	US-09-944-432-99	Sequence 99, Appl
c	19	12.2	61.0	20	10	US-09-943-762-99	Sequence 99, Appl
c	20	12.2	61.0	20	10	US-09-944-654-99	Sequence 99, Appl
c	21	12.2	61.0	20	10	US-09-943-851A-99	Sequence 99, Appl
	22	12.2	61.0	28	10	US-09-835-381-11	Sequence 11, Appl
	23	12	60.0	26	9	US-09-089-818B-5	Sequence 5, Appli
c	24	11.8	59.0	20	10	US-09-454-394-61	Sequence 61, Appl
	25	11.8	59.0	20	10	US-09-454-394-64	Sequence 64, Appl
c	26	11.8	59.0	20	10	US-09-791-406-75	Sequence 75, Appl
	27	11.8	59.0	35	10	US-09-867-569-5	Sequence 5, Appli
c	28	11.8	59.0	49	10	US-09-781-902-28	Sequence 28, Appl
c	29	11.6	58.0	34	9	US-09-764-868-1247	Sequence 1247, Ap
c	30	11.4	57.0	16	10	US-09-781-902-52	Sequence 52, Appl
c	31	11.4	57.0	31	10	US-09-801-274-352	Sequence 352, App
	32	11.4	57.0	36	9	US-10-127-391-27	Sequence 27, Appl
	33	11.4	57.0	39	9	US-09-252-150-59	Sequence 59, Appl
	34	11.4	57.0	46	10	US-09-320-337-38	Sequence 38, Appl
	35	11.2	56.0	20	10	US-09-733-294A-38	Sequence 38, Appl
	36	11.2	56.0	20	10	US-09-733-294A-39	Sequence 39, Appl
c	37	11.2	56.0	25	9	US-09-978-295A-376	Sequence 376, App
c	38	11.2	56.0	25	9	US-09-978-697-376	Sequence 376, App
c	39	11.2	56.0	30	10	US-09-844-684-8	Sequence 8, Appli
	40	11	55.0	20	10	US-09-733-294A-65	Sequence 65, Appl
c	41	11	55.0	22	10	US-09-755-665-68	Sequence 68, Appl
	42	11	55.0	25	10	US-09-866-108-3303	Sequence 3303, Ap
	43	11	55.0	25	10	US-09-866-108-3304	Sequence 3304, Ap
	44	11	55.0	25	10	US-09-866-108-3305	Sequence 3305, Ap
	45	11	55.0	25	10	US-09-866-108-3306	Sequence 3306, Ap

ALIGNMENTS

RESULT 1
US-09-752-639-36
; Sequence 36, Application US/09752639
; Patent No. US20020091243A1
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; APPLICANT: Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
; TITLE OF INVENTION: of Use Thereof
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/752,639
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US99/10793
; FILING DATE:
; APPLICATION NUMBER: 09/081,385
; FILING DATE:
; APPLICATION NUMBER: 08/964,747
; FILING DATE: 05-NOV-1997
; APPLICATION NUMBER: 60/030,761
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wu, Frank
; REGISTRATION NUMBER: 41,386
; REFERENCE/DOCKET NUMBER: 22000-20577.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600

```
;       TELEFAX:  650-494-0792
;       TELEX:  706141
;   INFORMATION FOR SEQ ID NO:  36:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  20 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-09-752-639-36

  Query Match             72.0%;  Score 14.4;  DB 10;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCC 16
           ||||||||||||||| |
Db       1 GTTCCCAGAGCTTGTC 16


RESULT 2
US-09-984-198-36
; Sequence 36, Application US/09984198
; Patent No. US20020106679A1
;  GENERAL INFORMATION:
;    APPLICANT:  Gatanaga, T.
;    APPLICANT:  Granger, G.A.
;    TITLE OF INVENTION:  Factors Altering Tumor Necrosis
;    TITLE OF INVENTION:  Factor Receptor Releasing Enzyme Activity, and Methods
;    TITLE OF INVENTION:  of Use Thereof
;    NUMBER OF SEQUENCES:  154
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/984,198
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US99/10793
;      FILING DATE:
;      APPLICATION NUMBER:  09/081,385
;      FILING DATE:
;      APPLICATION NUMBER:  08/964,747
;      FILING DATE:  05-NOV-1997
;      APPLICATION NUMBER:  60/030,761
;      FILING DATE:  06-NOV-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wu, Frank
;      REGISTRATION NUMBER:  41,386
;      REFERENCE/DOCKET NUMBER:  22000-20577.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-813-5600
;      TELEFAX:  650-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-984-198-36

  Query Match             72.0%;  Score 14.4;  DB 10;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCC 16
           ||||||||||||||| |
Db       1 GTTCCCAGAGCTTGTC 16


RESULT 3
US-09-815-153-9
; Sequence 9, Application US/09815153
; Patent No. US20020132978A1
; GENERAL INFORMATION:
;  APPLICANT: RASTELLI, LUCA K.
;  APPLICANT:  GERBER, HANS-PETER
;  TITLE OF INVENTION: VEGF-MODULATED GENES AND METHODS EMPLOYING THEM
;  FILE REFERENCE: 10716/34
;  CURRENT APPLICATION NUMBER: US/09/815,153
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: 60/191,201
;  PRIOR FILING DATE: 2000-03-21
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-815-153-9

  Query Match             68.0%;  Score 13.6;  DB 10;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 4.7e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCCACCT 20
           ||||||| || |||||  ||
Db       4 GTTCCCAAAGTTTGCCGGCT 23


RESULT 4
US-09-801-274-992
; Sequence 992, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
;  APPLICANT: Cargill, Michele
;  APPLICANT:  Ireland, James S.
;  APPLICANT:  Lander, Eric S.
;  TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
;  FILE REFERENCE: 2825.2009-001
;  CURRENT APPLICATION NUMBER: US/09/801,274
;  CURRENT FILING DATE:  2001-03-07
;  PRIOR APPLICATION NUMBER: US 60/187,510
;  PRIOR FILING DATE: 2000-03-07
;  PRIOR APPLICATION NUMBER: US 60/206,129
;  PRIOR FILING DATE: 2000-05-22
;  NUMBER OF SEQ ID NOS: 1802
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 992
;   LENGTH: 31
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-801-274-992

  Query Match             66.0%;  Score 13.2;  DB 10;  Length 31;
  Best Local Similarity   75.0%;  Pred. No. 7.6e+02;
  Matches   15;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCCACCT 20
           ||||| :|||||   |||||
Db      10 GTTCCGRGAGCTGCTCACCT 29


RESULT 5
```

```
US-09-841-366A-33
; Sequence 33, Application US/09841366A
; Patent No. US20020058265A1
; GENERAL INFORMATION:
;  APPLICANT: Bacher, Jeffery W.
;  APPLICANT: Flanagan, Laura
;  APPLICANT: Nassif, Nadine
;  TITLE OF INVENTION: DETECTION OF MICROSATELLITE INSTABILITY AND ITS USE IN
;  TITLE OF INVENTION: DIAGNOSIS OF TUMORS
;  FILE REFERENCE: 16026-9267
;  CURRENT APPLICATION NUMBER: US/09/841,366A
;  CURRENT FILING DATE: 2001-07-16
;  PRIOR APPLICATION NUMBER: 09/663,020
;  PRIOR FILING DATE: 2000-09-15
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: D9S2169 primer
US-09-841-366A-33

  Query Match             63.0%;  Score 12.6;  DB 10;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 1.4e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2 TTCCCAGAGCTTGCCACCT 20
           |||||| |  |||||| ||
Db       1 TTCCCAAAAGTTGCCATCT 19


RESULT 6
US-09-216-393-289
; Sequence 289, Application US/09216393
; Patent No. US20010014447A1
; GENERAL INFORMATION:
;  APPLICANT: Milhausen, Michael James
;  TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND
;  TITLE OF INVENTION: USES THEREOF
;  FILE REFERENCE: TX-1-C2
;  CURRENT APPLICATION NUMBER: US/09/216,393
;  CURRENT FILING DATE: 1998-12-18
;  EARLIER APPLICATION NUMBER: 08/994,825
;  EARLIER FILING DATE: 1997-12-19
;  NUMBER OF SEQ ID NOS: 364
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 289
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-09-216-393-289

  Query Match             62.0%;  Score 12.4;  DB 10;  Length 19;
  Best Local Similarity   92.9%;  Pred. No. 1.8e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 TTCCCAGAGCTTGC 15
           |||||||| |||||
Db       2 TTCCCAGACCTTGC 15


RESULT 7
US-09-944-413-99/c
; Sequence 99, Application US/09944413
; Patent No. US20020156004A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/944,413
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/067,411
;  PRIOR FILING DATE: December 3, 1997
;  PRIOR APPLICATION NUMBER: 60/069,334
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,278
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,425
;  PRIOR FILING DATE: December 12, 1997
;  PRIOR APPLICATION NUMBER: 60/069,696
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,694
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,702
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,870
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/069,873
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/068,017
;  PRIOR FILING DATE: December 18, 1997
;  PRIOR APPLICATION NUMBER: 60/070,440
;  PRIOR FILING DATE: January 5, 1998
;  PRIOR APPLICATION NUMBER: 60/074,086
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/074,092
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/075,945
;  PRIOR FILING DATE: February 25, 1998
;  PRIOR APPLICATION NUMBER: 60/112,850
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 60/113,296
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
;  PRIOR APPLICATION NUMBER: PCT/US98/19330
;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
;  PRIOR APPLICATION NUMBER: 09/216,021
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 09/218,517
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 09/254,311
;  PRIOR FILING DATE: March 3, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: June 22, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: September 15, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28409
;  PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
```

```
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: No. US20020156004Alember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28301
;  PRIOR FILING DATE: Decemberl, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: December 16, 1999
;  PRIOR APPLICATION NUMBER: PCT/US00/03565
;  PRIOR FILING DATE: February 11, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: February 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: March 2, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: March 30, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: May 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/20710
;  PRIOR FILING DATE: July 28, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: December 1, 2000
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: February 28, 2001
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 99
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-413-99

  Query Match             61.0%;  Score 12.2;  DB 9;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCCA 17
           ||||||| |||||||
Db      17 GTTCCCATTCCTTGCCA 1


RESULT 8
US-09-944-403-99/c
; Sequence 99, Application US/09944403
; Patent No. US20020165143A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/944,403
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/067,411
;  PRIOR FILING DATE: December 3, 1997
;  PRIOR APPLICATION NUMBER: 60/069,334
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,278
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,425
;  PRIOR FILING DATE: December 12, 1997
;  PRIOR APPLICATION NUMBER: 60/069,696
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,694
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,702
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,870
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/069,873
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/068,017
;  PRIOR FILING DATE: December 18, 1997
;  PRIOR APPLICATION NUMBER: 60/070,440
;  PRIOR FILING DATE: January 5, 1998
;  PRIOR APPLICATION NUMBER: 60/074,086
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/074,092
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/075,945
;  PRIOR FILING DATE: February 25, 1998
;  PRIOR APPLICATION NUMBER: 60/112,850
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 60/113,296
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
;  PRIOR APPLICATION NUMBER: PCT/US98/19330
;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
;  PRIOR APPLICATION NUMBER: 09/216,021
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 09/218,517
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 09/254,311
;  PRIOR FILING DATE: March 3, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: June 22, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: September 15, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28409
;  PRIOR FILING DATE: No. US20020165143Alember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: No. US20020165143Alember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28301
;  PRIOR FILING DATE: Decemberl, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: December 16, 1999
;  PRIOR APPLICATION NUMBER: PCT/US00/03565
;  PRIOR FILING DATE: February 11, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: February 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: March 2, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: March 30, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: May 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/20710
;  PRIOR FILING DATE: July 28, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: December 1, 2000
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: February 28, 2001
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 99
;   LENGTH: 20
;   TYPE: DNA
```

```
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-403-99

  Query Match             61.0%;  Score 12.2;  DB 9;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 GTTCCCAGAGCTTGCCA 17
          |||||||   |||||||
Db     17 GTTCCCATTCCTTGCCA 1


RESULT 9
US-09-944-896-99/c
; Sequence 99, Application US/09944896
; Patent No. US20020168715A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/944,896
;  CURRENT FILING DATE:  2001-08-31
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/069,334
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,278
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,425
;  PRIOR FILING DATE: December 12, 1997
;  PRIOR APPLICATION NUMBER: 60/069,696
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,694
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,702
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,870
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/069,873
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/068,017
;  PRIOR FILING DATE: December 18, 1997
;  PRIOR APPLICATION NUMBER: 60/070,440
;  PRIOR FILING DATE: January 5, 1998
;  PRIOR APPLICATION NUMBER: 60/074,086
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/074,092
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/075,945
;  PRIOR FILING DATE: February 25, 1998
;  PRIOR APPLICATION NUMBER: 60/112,850
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 60/113,296
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
;  PRIOR APPLICATION NUMBER: PCT/US98/19330
;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
;  PRIOR APPLICATION NUMBER: 09/216,021
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 09/218,517
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 09/254,311
;  PRIOR FILING DATE: March 3, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: June 22, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: September 15, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28409
;  PRIOR FILING DATE: No. US20020168715Alember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: No. US20020168715Alember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28301
;  PRIOR FILING DATE: December1, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: December 16, 1999
;  PRIOR APPLICATION NUMBER: PCT/US00/03565
;  PRIOR FILING DATE: February 11, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: February 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: March 2, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: March 30, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: May 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/20710
;  PRIOR FILING DATE: July 28, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: December 1, 2000
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: February 28, 2001
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 99
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-896-99

  Query Match             61.0%;  Score 12.2;  DB 9;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 GTTCCCAGAGCTTGCCA 17
          |||||||   |||||||
Db     17 GTTCCCATTCCTTGCCA 1


RESULT 10
US-09-944-944-99/c
; Sequence 99, Application US/09944944
; Patent No. US20020173463A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
```

```
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/944,944
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/067,411
;  PRIOR FILING DATE: December 3, 1997
;  PRIOR APPLICATION NUMBER: 60/069,334
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,278
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,425
;  PRIOR FILING DATE: December 12, 1997
;  PRIOR APPLICATION NUMBER: 60/069,696
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,694
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,702
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,870
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/069,873
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/068,017
;  PRIOR FILING DATE: December 18, 1997
;  PRIOR APPLICATION NUMBER: 60/070,440
;  PRIOR FILING DATE: January 5, 1998
;  PRIOR APPLICATION NUMBER: 60/074,086
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/074,092
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/075,945
;  PRIOR FILING DATE: February 25, 1998
;  PRIOR APPLICATION NUMBER: 60/112,850
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 60/113,296
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
;  PRIOR APPLICATION NUMBER: PCT/US98/19330
;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
;  PRIOR APPLICATION NUMBER: 09/216,021
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 09/218,517
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 09/254,311
;  PRIOR FILING DATE: March 3, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: June 22, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: September 15, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28409
;  PRIOR FILING DATE: No. US20020173463Alember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: No. US20020173463Alember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28301
;  PRIOR FILING DATE: December1, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: December 16, 1999
;  PRIOR APPLICATION NUMBER: PCT/US00/03565
;  PRIOR FILING DATE: February 11, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: February 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: March 2, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: March 30, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: May 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/20710
;  PRIOR FILING DATE: July 28, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: December 1, 2000
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: February 28, 2001
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 99
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-944-99

  Query Match             61.0%;  Score 12.2;  DB 9;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCCA 17
           |||||||   |||||||
Db      17 GTTCCCATTCCTTGCCA 1


RESULT 11
US-09-866-028-99/c
; Sequence 99, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/866,028
;  CURRENT FILING DATE:  2001-05-25
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 99
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-866-028-99

  Query Match             61.0%;  Score 12.2;  DB 10;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy       1 GTTCCCAGAGCTTGCCA 17
           ||||||| |||||||
Db      17 GTTCCCATTCCTTGCCA 1


RESULT 12
US-09-944-449-99/c
; Sequence 99, Application US/09944449
; Patent No. US20020102647A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/944,449
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/067,411
;  PRIOR FILING DATE: December 3, 1997
;  PRIOR APPLICATION NUMBER: 60/069,334
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,278
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,425
;  PRIOR FILING DATE: December 12, 1997
;  PRIOR APPLICATION NUMBER: 60/069,696
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,694
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,702
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,870
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/069,873
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/068,017
;  PRIOR FILING DATE: December 18, 1997
;  PRIOR APPLICATION NUMBER: 60/070,440
;  PRIOR FILING DATE: January 5, 1998
;  PRIOR APPLICATION NUMBER: 60/074,086
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/074,092
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/075,945
;  PRIOR FILING DATE: February 25, 1998
;  PRIOR APPLICATION NUMBER: 60/112,850
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 60/113,296
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
;  PRIOR APPLICATION NUMBER: PCT/US98/19330
;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
;  PRIOR APPLICATION NUMBER: 09/216,021
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 09/218,517
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 09/254,311
;  PRIOR FILING DATE: March 3, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: June 22, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: September 15, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28409
;  PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28301
;  PRIOR FILING DATE: Decemberl, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: December 16, 1999
;  PRIOR APPLICATION NUMBER: PCT/US00/03565
;  PRIOR FILING DATE: February 11, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: February 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: March 2, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: March 30, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: May 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/20710
;  PRIOR FILING DATE: July 28, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: December 1, 2000
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: February 28, 2001
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 99
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-449-99

  Query Match             61.0%;  Score 12.2;  DB 10;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCCA 17
           ||||||| |||||||
Db      17 GTTCCCATTCCTTGCCA 1


RESULT 13
US-09-944-457-99/c
; Sequence 99, Application US/09944457
; Patent No. US20020110859A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
```

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020110859Alember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020110859Alember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 99
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-457-99

Query Match 61.0%; Score 12.2; DB 10; Length 20;
Best Local Similarity 82.4%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels ÷ 0; Gaps 0;

Qy 1 GTTCCCAGAGCTTGCCA 17
||||||| |||||||
Db 17 GTTCCCATTCCTTGCCA 1

RESULT 14
US-09-945-587-99/c
; Sequence 99, Application US/09945587
; Patent No. US20020127643A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,587
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873

```
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/068,017
;  PRIOR FILING DATE: December 18, 1997
;  PRIOR APPLICATION NUMBER: 60/070,440
;  PRIOR FILING DATE: January 5, 1998
;  PRIOR APPLICATION NUMBER: 60/074,086
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/074,092
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/075,945
;  PRIOR FILING DATE: February 25, 1998
;  PRIOR APPLICATION NUMBER: 60/112,850
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 60/113,296
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
;  PRIOR APPLICATION NUMBER: PCT/US98/19330
;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
;  PRIOR APPLICATION NUMBER: 09/216,021
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 09/218,517
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 09/254,311
;  PRIOR FILING DATE: March 3, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: June 22, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: September 15, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28409
;  PRIOR FILING DATE: No. US20020127643A1ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: No. US20020127643A1ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28301
;  PRIOR FILING DATE: December1, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: December 16, 1999
;  PRIOR APPLICATION NUMBER: PCT/US00/03565
;  PRIOR FILING DATE: February 11, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: February 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: March 2, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: March 30, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: May 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/20710
;  PRIOR FILING DATE: July 28, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: December 1, 2000
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: February 28, 2001
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 99
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-945-587-99

  Query Match             61.0%;  Score 12.2;  DB 10;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCCA 17
           ||||||| |||||||
Db      17 GTTCCCATTCCTTGCCA 1
```

```
RESULT 15
US-09-945-015-99/c
; Sequence 99, Application US/09945015
; Patent No. US20020132768A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/945,015
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/067,411
;  PRIOR FILING DATE: December 3, 1997
;  PRIOR APPLICATION NUMBER: 60/069,334
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,278
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,425
;  PRIOR FILING DATE: December 12, 1997
;  PRIOR APPLICATION NUMBER: 60/069,696
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,694
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,702
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,870
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/069,873
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/068,017
;  PRIOR FILING DATE: December 18, 1997
;  PRIOR APPLICATION NUMBER: 60/070,440
;  PRIOR FILING DATE: January 5, 1998
;  PRIOR APPLICATION NUMBER: 60/074,086
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/074,092
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/075,945
;  PRIOR FILING DATE: February 25, 1998
;  PRIOR APPLICATION NUMBER: 60/112,850
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 60/113,296
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
;  PRIOR APPLICATION NUMBER: PCT/US98/19330
;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
;  PRIOR APPLICATION NUMBER: 09/216,021
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 09/218,517
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 09/254,311
```

```
;  PRIOR FILING DATE: March 3, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: June 22, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: September 15, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28409
;  PRIOR FILING DATE: No. US20020132768Alember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: No. US20020132768Alember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28301
;  PRIOR FILING DATE: December1, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: December 16, 1999
;  PRIOR APPLICATION NUMBER: PCT/US00/03565
;  PRIOR FILING DATE: February 11, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: February 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: March 2, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: March 30, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: May 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/20710
;  PRIOR FILING DATE: July 28, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: December 1, 2000
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: February 28, 2001
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 99
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-945-015-99

  Query Match             61.0%;  Score 12.2;  DB 10;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCCA 17
           |||||||   |||||||
Db      17 GTTCCCATTCCTTGCCA 1


Search completed: November 28, 2002, 19:35:04
Job time : 43.069 secs
```

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 17:12:29 ; Search time 40.3448 Seconds
(without alignments)
152.028 Million cell updates/sec

Title: US-09-719-737-2
Perfect score: 20
Sequence: 1 gttcccagagcttgccacct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13.4	67.0	17	3	US-08-998-099-89	Sequence 89, Appl
c	2	13.4	67.0	20	4	US-09-476-256-5	Sequence 5, Appli
c	3	13.4	67.0	20	4	US-09-476-256-11	Sequence 11, Appl
c	4	13.4	67.0	20	4	US-09-844-634-158	Sequence 158, App
c	5	13.2	66.0	45	6	5395760-9	Patent No. 5395760
	6	13	65.0	35	4	US-09-039-198A-21	Sequence 21, Appl
	7	13	65.0	35	4	US-09-267-574-21	Sequence 21, Appl
c	8	12.4	62.0	38	3	US-09-023-082A-40	Sequence 40, Appl
	9	12.2	61.0	18	3	US-09-344-579-22	Sequence 22, Appl
	10	12.2	61.0	19	1	US-08-358-782D-5	Sequence 5, Appli
	11	12.2	61.0	19	2	US-08-764-527A-5	Sequence 5, Appli
	12	12.2	61.0	24	1	US-08-066-325-5	Sequence 5, Appli
	13	12.2	61.0	28	3	US-08-483-316-5	Sequence 5, Appli
	14	12.2	61.0	28	4	US-08-500-306-1	Sequence 1, Appli
	15	12.2	61.0	28	4	US-09-521-668B-7	Sequence 7, Appli
	16	12.2	61.0	28	5	PCT-US95-12624-5	Sequence 5, Appli
c	17	12.2	61.0	33	1	US-07-951-715A-59	Sequence 59, Appl
c	18	12.2	61.0	33	2	US-08-459-448A-59	Sequence 59, Appl
c	19	12.2	61.0	33	3	US-08-459-595A-59	Sequence 59, Appl
c	20	12.2	61.0	33	3	US-08-459-504B-59	Sequence 59, Appl
c	21	12.2	61.0	33	3	US-08-459-444-59	Sequence 59, Appl
c	22	12.2	61.0	33	4	US-09-547-422-59	Sequence 59, Appl
	23	12.2	61.0	35	3	US-08-435-568A-33	Sequence 33, Appl
	24	12.2	61.0	41	3	US-08-483-316-7	Sequence 7, Appli
	25	12.2	61.0	41	5	PCT-US95-12624-7	Sequence 7, Appli
	26	12	60.0	26	2	US-08-887-997B-5	Sequence 5, Appli
c	27	12	60.0	27	1	US-08-434-503-41	Sequence 41, Appl
	28	12	60.0	34	4	US-09-432-020B-41	Sequence 41, Appl
	29	12	60.0	42	1	US-07-834-539A-13	Sequence 13, Appl
	30	12	60.0	42	1	US-08-053-131-21	Sequence 21, Appl
	31	12	60.0	42	1	US-08-053-131-65	Sequence 65, Appl
	32	12	60.0	42	1	US-08-645-641-21	Sequence 21, Appl
	33	12	60.0	42	1	US-08-645-641-65	Sequence 65, Appl
	34	12	60.0	42	1	US-07-853-408B-21	Sequence 21, Appl
	35	12	60.0	42	1	US-07-853-408B-65	Sequence 65, Appl
	36	12	60.0	42	1	US-08-096-762-21	Sequence 21, Appl
	37	12	60.0	42	1	US-08-096-762-65	Sequence 65, Appl
	38	12	60.0	42	2	US-08-800-353-13	Sequence 13, Appl
	39	12	60.0	42	2	US-08-308-865-21	Sequence 21, Appl
	40	12	60.0	42	2	US-08-308-865-65	Sequence 65, Appl
	41	12	60.0	42	4	US-09-042-353-189	Sequence 189, App
	42	12	60.0	42	4	US-09-042-353-226	Sequence 226, App
	43	12	60.0	42	4	US-08-758-417A-37	Sequence 37, Appl
	44	12	60.0	42	4	US-08-758-417A-74	Sequence 74, Appl
	45	12	60.0	42	5	PCT-US92-06185-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-998-099-89
; Sequence 89, Application US/08998099A
; Patent No. 6103890
; GENERAL INFORMATION:
; APPLICANT: JARVIS, THALE
; APPLICANT: MCSWIGGEN, JAMES A.
; APPLICANT: STINCHCOMB, DAN T.
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
; FILE REFERENCE: 231/175
; CURRENT APPLICATION NUMBER: US/08/998,099A
; CURRENT FILING DATE: 1997-12-24
; EARLIER APPLICATION NUMBER: 60/037,658
; EARLIER FILING DATE: 1997-01-23
; EARLIER APPLICATION NUMBER: 08/373,124
; EARLIER FILING DATE: 1995-01-13
; EARLIER APPLICATION NUMBER: 08/245,466
; EARLIER FILING DATE: 1994-05-18
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 89
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-08-998-099-89

Query Match 67.0%; Score 13.4; DB 3; Length 17;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy       5 CCAGAGCTTGCCACC 19
           |||||| ::||||||
Db       1 CCAGAGGUUGCCACC 15
```

RESULT 2
US-09-476-256-5/c
; Sequence 5, Application US/09476256
; Patent No. 6228592
; GENERAL INFORMATION:
; APPLICANT: Laboratory of Molecular Biophotonics
; TITLE OF INVENTION: Nucleic Acid Detection in Cytoplasm
; FILE REFERENCE: BBP99-02
; CURRENT APPLICATION NUMBER: US/09/476,256
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA

```
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: probe
US-09-476-256-5

  Query Match             67.0%;  Score 13.4;  DB 4;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 CCAGAGCTTGCCACC 19
           |||||| ||||||||
Db      20 CCAGAGGTTGCCACC 6


RESULT 3
US-09-476-256-11/c
; Sequence 11, Application US/09476256
; Patent No. 6228592
; GENERAL INFORMATION:
;  APPLICANT: Laboratory of Molecular Biophotonics
;  TITLE OF INVENTION: Nucleic Acid Detection in Cytoplasm
;  FILE REFERENCE: BBP99-02
;  CURRENT APPLICATION NUMBER: US/09/476,256
;  CURRENT FILING DATE: 1999-12-30
;  NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 11
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: probe
US-09-476-256-11

  Query Match             67.0%;  Score 13.4;  DB 4;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 CCAGAGCTTGCCACC 19
           |||||| ||||||||
Db      20 CCAGAGGTTGCCACC 6


RESULT 4
US-09-844-634-158/c
; Sequence 158, Application US/09844634
; Patent No. 6410324
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2 EXPRESSI
;  FILE REFERENCE: RTS-0216
;  CURRENT APPLICATION NUMBER: US/09/844,634
;  CURRENT FILING DATE:  2001-04-27
;  NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 158
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-844-634-158

  Query Match             67.0%;  Score 13.4;  DB 4;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGC 15
           || ||||||||||||
Db      15 GTACCCAGAGCTTGC 1


RESULT 5
5395760-9/c
;Patent No. 5395760
;    APPLICANT: SMITH, CRAIG A.;GOODWIN, RAYMOND G.;BECKMANN,
;M. PATRICIA
;    TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
;B-RECEPTORS
;    NUMBER OF SEQUENCES: 17
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/523,635
;      FILING DATE: 10-MAY-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 421,417
;      FILING DATE: 13-OCT-1989
;      APPLICATION NUMBER: 405,370
;      FILING DATE: 11-SEP-1989
;      APPLICATION NUMBER: 403,241
;      FILING DATE: 05-SEP-1989
;SEQ ID NO:9:
;      LENGTH: 45
5395760-9

  Query Match             66.0%;  Score 13.2;  DB 6;  Length 45;
  Best Local Similarity   83.3%;  Pred. No. 5.3e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 TTCCCAGAGCTTGCCACC 19
           ||||||| | | ||||||
Db      30 TTCCCAGGGATGGCCACC 13


RESULT 6
US-09-039-198A-21
; Sequence 21, Application US/09039198A
; Patent No. 6200951
;  GENERAL INFORMATION:
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Tjoelker, Larry W.
;    TITLE OF INVENTION:  CHITINASE CHITIN-BINDING FRAGMENTS
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  233 South Wacker Drive/6300 Sears Tower
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/039,198A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rin-Laures, Li-Hsien
;      REGISTRATION NUMBER:  33,547
;      REFERENCE/DOCKET NUMBER:  27866/34391
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "primer"
US-09-039-198A-21

  Query Match             65.0%;  Score 13;  DB 4;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+02;
```

```
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TTCCCAGAGCTTG 14
           |||||||||||||
Db       8 TTCCCAGAGCTTG 20


RESULT 7
US-09-267-574-21
; Sequence 21, Application US/09267574
; Patent No. 6399571
; GENERAL INFORMATION:
;  APPLICANT: Gray, Patrick W.
;  APPLICANT: Tjoelker, Larry W.
;  TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
;  FILE REFERENCE: 27866/35407
;  CURRENT APPLICATION NUMBER: US/09/267,574
;  CURRENT FILING DATE: 1999-03-12
;  EARLIER APPLICATION NUMBER: 09/039,198
;  EARLIER FILING DATE: 1998-03-12
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
;   LENGTH: 35
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-267-574-21

  Query Match             65.0%;  Score 13;  DB 4;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TTCCCAGAGCTTG 14
           |||||||||||||
Db       8 TTCCCAGAGCTTG 20


RESULT 8
US-09-023-082A-40/c
; Sequence 40, Application US/09023082A
; Patent No. 6077692
;  GENERAL INFORMATION:
;    APPLICANT:  RUBEN, STEVEN M.
;    APPLICANT:  JIMENEZ, PABLO
;    APPLICANT:  DUAN, D. ROXANNE
;    APPLICANT:  RAMPY, MARK A.
;    APPLICANT:  MENDRICK, DONNA
;    APPLICANT:  ZHANG, JUN
;    APPLICANT:  NI, JIAN
;    APPLICANT:  MOORE, PAUL A.
;    APPLICANT:  COLEMAN, TIMOTHY A.
;    APPLICANT:  GRUBER, JOACHIM R.
;    APPLICANT:  DILLON, PATRICK J.
;    APPLICANT:  GENTZ, REINER L.
;    TITLE OF INVENTION:  KERATINOCYTE GROWTH FACTOR-2
;    NUMBER OF SEQUENCES:  148
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;      STREET:  1100 NEW YORK AVE, NW, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,082A
;      FILING DATE:  13-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01790
;      FILING DATE:  14-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/461,195
;      FILING DATE:  05-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/023,852
;      FILING DATE:  13-AUG-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,045
;      FILING DATE:  28-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/862,432
;      FILING DATE:  23-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/910,875
;      FILING DATE:  13-AUG-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/055,561
;      FILING DATE:  13-AUG-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  STEFFFE, ERIC K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0360008/EKS
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  38 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-023-082A-40

  Query Match             62.0%;  Score 12.4;  DB 3;  Length 38;
  Best Local Similarity   92.9%;  Pred. No. 1.3e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 CCCAGAGCTTGCCA 17
           |||||||||| ||
Db      24 CCCAGAGCTTGACA 11


RESULT 9
US-09-344-579-22
; Sequence 22, Application US/09344579
; Patent No. 6054316
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF ETS-2 EXPRESSION
;  FILE REFERENCE: RTS-0063
;  CURRENT APPLICATION NUMBER: US/09/344,579
;  CURRENT FILING DATE: 1999-06-25
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 22
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-344-579-22

  Query Match             61.0%;  Score 12.2;  DB 3;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 1.5e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCCA 17
           |||||||||| || ||
```

```
Db      2 GTTCCCAGAGAATGTCA 18


RESULT 10
US-08-358-782D-5
; Sequence 5, Application US/08358782D
; Patent No. 5674682
;  GENERAL INFORMATION:
;    APPLICANT:  Croce, Carlo
;    APPLICANT:  Gomella, Leonard
;    APPLICANT:  Mulholland, S. Grant
;    APPLICANT:  Moreno, Jose
;    APPLICANT:  Fischer, Rainer
;    TITLE OF INVENTION:  Methods of Detecting Micrometastasis of Prostate
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz &
;      STREET:  One Liberty Place 46th. Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/358,782D
;      FILING DATE:  15-DEC-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Beardell, Lori Y.
;      REGISTRATION NUMBER:  34,293
;      REFERENCE/DOCKET NUMBER:  TJU-1327
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-358-782D-5

  Query Match             61.0%;  Score 12.2;  DB 1;  Length 19;
  Best Local Similarity   82.4%;  Pred. No. 1.5e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      4 CCCAGAGCTTGCCACCT 20
          |||  ||||| ||||||
Db      3 CCCCAAGCTTACCACCT 19


RESULT 11
US-08-764-527A-5
; Sequence 5, Application US/08764527A
; Patent No. 5939258
;  GENERAL INFORMATION:
;    APPLICANT:  Croce, Carlo
;    APPLICANT:  Gomella, Leonard
;    APPLICANT:  Mulholland, S. Grant
;    APPLICANT:  Moreno, Jose
;    APPLICANT:  Fischer, Rainer
;    TITLE OF INVENTION:  Methods of Detecting Micrometastasis of
;    TITLE OF INVENTION:  Prostate
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz &
;      STREET:  One Liberty Place 46th. Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/764,527A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/358,782
;      FILING DATE:  15-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Beardell, Lori Y.
;      REGISTRATION NUMBER:  34,293
;      REFERENCE/DOCKET NUMBER:  TJU-1327
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-764-527A-5

  Query Match             61.0%;  Score 12.2;  DB 2;  Length 19;
  Best Local Similarity   82.4%;  Pred. No. 1.5e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      4 CCCAGAGCTTGCCACCT 20
          |||  ||||| ||||||
Db      3 CCCCAAGCTTACCACCT 19


RESULT 12
US-08-066-325-5
; Sequence 5, Application US/08066325
; Patent No. 5667967
;  GENERAL INFORMATION:
;    APPLICANT:  Steinman, Lawrence
;    APPLICANT:  Oksenberg, Jorge
;    APPLICANT:  Bernard, Claude
;    TITLE OF INVENTION:  T-CELL RECEPTOR VARIABLE TRANSCRIPTS AS DISEASE RELATED MAR
;    NUMBER OF SEQUENCES:  157
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  .SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/066,325
;      FILING DATE:  21-MAY-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5667967tenburg Ph.D., Carol
;      REGISTRATION NUMBER:  39,317
;      REFERENCE/DOCKET NUMBER:  690068.408C1
;    TELECOMMUNICATION INFORMATION:
```

```
;       TELEPHONE:  (206) 622-4900
;       TELEFAX:  (206) 682-6031
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  24 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-066-325-5

  Query Match             61.0%;  Score 12.2;  DB 1;  Length 24;
  Best Local Similarity   82.4%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCCA 17
           ||||||||||   ||||
Db       3 GTTCCCAGAGGGAGCCA 19


RESULT 13
US-08-483-316-5
; Sequence 5, Application US/08483316
; Patent No. 6045802
;  GENERAL INFORMATION:
;     APPLICANT:  SCHLOM, JEFFREY
;     APPLICANT:  KANTOR, JUDITH
;     TITLE OF INVENTION:  ENHANCED IMMUNE RESPONSE
;     TITLE OF INVENTION:  TO AN ANTIGEN BY A COMPOSITION OF A
;     TITLE OF INVENTION:  RECOMBINANT VIRUS EXPRESSING THE ANTIGEN WITH
;     TITLE OF INVENTION:  A RECOMBINANT VIRUS EXPRESSING AN IMMUNO-
;     NUMBER OF SEQUENCES:  9
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  MORGAN & FINNEGAN, L.L.P.
;       STREET:  345 PARK AVENUE
;       CITY:  NEW YORK
;       STATE:  NEW YORK
;       COUNTRY:  USA
;       ZIP:  10154
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.50 INCH, 1.44 Mb STORAGE
;       COMPUTER:  IBM PC COMPATIBLE
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WORDPERFECT 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/483,316
;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/317,268
;       FILING DATE:  03-OCT-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BROWN, KATHRYN M.
;       REGISTRATION NUMBER:  34,556
;       REFERENCE/DOCKET NUMBER:  2026-4176US1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 758-4800
;       TELEFAX:  (212) 751-6849
;       TELEX:  421792
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  28 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;     HYPOTHETICAL:  Yes
;     ANTI-SENSE:  No
US-08-483-316-5

  Query Match             61.0%;  Score 12.2;  DB 3;  Length 28;
  Best Local Similarity   82.4%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4 CCCAGAGCTTGCCACCT 20
           |||  |||||  ||||||
Db       9 CCCCAAGCTTACCACCT 25


RESULT 14
US-08-500-306-1
; Sequence 1, Application US/08500306
; Patent No. 6165460
;  GENERAL INFORMATION:
;     APPLICANT:  SCHLOM, JEFFREY
;     APPLICANT:  PANICALI, DENNIS
;     TITLE OF INVENTION:  GENERATION OF IMMUNE RESPONSES TO
;     TITLE OF INVENTION:  PROSTATE-SPECIFIC ANTIGEN (PSA)
;     NUMBER OF SEQUENCES:  2
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SEWALL P. BRONSTEIN; DIKE, BRONSTEIN,
;       ADDRESSEE:  ROBERTS & CUSHMAN
;       STREET:  130 WATER STREET
;       CITY:  BOSTON
;       STATE:  MASSACHUSETTS
;       COUNTRY:  US
;       ZIP:  02129
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/500,306
;       FILING DATE:
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  RESNICK, DAVID S.
;       REGISTRATION NUMBER:  34,235
;       REFERENCE/DOCKET NUMBER:  44981
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 523-3400
;       TELEFAX:  (617) 523-6440
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  28 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  unknown
;       TOPOLOGY:  unknown
US-08-500-306-1

  Query Match             61.0%;  Score 12.2;  DB 4;  Length 28;
  Best Local Similarity   82.4%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4 CCCAGAGCTTGCCACCT 20
           |||  |||||  ||||||
Db       9 CCCCAAGCTTACCACCT 25


RESULT 15
US-09-521-668B-7
; Sequence 7, Application US/09521668B
; Patent No. 6303383
; GENERAL INFORMATION:
;  APPLICANT:  NAKAMURA, JUN
;  APPLICANT:  KANNO, SOHEI
;  APPLICANT:  KIMURA, EIICHIRO
;  APPLICANT:  MATSUI, KAUHIKO
;  APPLICANT:  NAKAMATSU, TSUYOSHI
;  TITLE OF INVENTION:  TEMPERATURE SENSITIVE PLASMID FOR CORYNEFORM BACTERIA
;  FILE REFERENCE:  0010-1093-0
;  CURRENT APPLICATION NUMBER: US/09/521,668B
;  CURRENT FILING DATE:  2000-03-08
;  PRIOR APPLICATION NUMBER:  JP 11-69896
;  PRIOR FILING DATE:  1999-03-16
;  NUMBER OF SEQ ID NOS:  20
```

```
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 28
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: completely synthesized
US-09-521-668B-7

  Query Match            61.0%;  Score 12.2;  DB 4;  Length 28;
  Best Local Similarity  82.4%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 TTCCCAGAGCTTGCCAC 18
           | ||  ||||||||||
Db       4 TCCCGGGAGCTTGCCAC 20


Search completed: November 28, 2002, 19:32:49
Job time : 41.3448 secs
```

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 15:32:44 ; Search time 185.517 Seconds
(without alignments)
242.780 Million cell updates/sec

Title: US-09-719-737-2
Perfect score: 20
Sequence: 1 gttcccagagcttgccacct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20	100.0	20	21	AAZ56186	Antisense oligonuc
c 2		13.8	69.0	17	21	AAC73582	Reverse primer #12
3		13.6	68.0	25	22	AAI67449	Probe sequence use
4		13.6	68.0	25	22	AAH22292	Tissue factor path
5		13.4	67.0	17	19	AAV95349	Human c-fos target
c 6		13.4	67.0	20	22	AAC83618	Human c-fos oligo
c 7		13.4	67.0	20	22	AAC83624	Human c-fos Bodipy
8		13.2	66.0	20	24	ABI95431	Capture oligonucle
9		13.2	66.0	24	24	ABI87432	Capture oligonucle
c 10		13.2	66.0	24	24	ABI87433	Capture oligonucle
11		13.2	66.0	24	24	ABI88068	Capture oligonucle
c 12		13.2	66.0	24	24	ABI88069	Capture oligonucle
13		13.2	66.0	28	10	AAN91567	Neisseria gonorrho
14		13.2	66.0	28	10	AAN91568	Neisseria gonorrho
c 15		13.2	66.0	28	10	AAN91569	Neisseria gonorrho
c 16		13.2	66.0	28	10	AAN91570	Neisseria gonorrho
c 17		13	65.0	15	22	AAF69386	Human IL4Ralpha ge
18		13	65.0	35	20	AAZ20957	Primer SEAP CBD 12
19		12.8	64.0	24	24	ABK16391	Mouse adipose prot
20		12.8	64.0	25	21	AAA57806	Antisense oligonuc
21		12.8	64.0	26	24	ABQ75836	Oligonucleotide fo
22		12.8	64.0	41	24	ABA97869	Human NPAT protein
23		12.8	64.0	44	20	AAX26321	PCR primer used to
c 24		12.8	64.0	50	22	AAI77541	Human silent SNP c
25		12.6	63.0	20	24	AAD38348	Human D9S2169 locu
26		12.6	63.0	20	24	AAD36387	Human D9S2169 loci
27		12.6	63.0	21	22	AAF97155	Human gene single
c 28		12.6	63.0	25	22	AAF83960	BAP28 gene fragmen
c 29		12.6	63.0	28	21	AAA08335	Spinach chloroplas
c 30		12.6	63.0	39	20	AAX55433	Soluble sc-TCR fus
31		12.4	62.0	19	20	AAX91414	T. gondii MGIS4-4
32		12.4	62.0	19	22	AAS42737	Sequencing primer
33		12.4	62.0	21	22	AAF96776	Human gene single
34		12.4	62.0	29	21	AAA04539	Polymorphic fragme
c 35		12.4	62.0	32	24	AAI67624	P. patens cell cyc
c 36		12.4	62.0	32	24	AAI67632	Cell cycle (CC-2)
c 37		12.4	62.0	38	19	AAV19998	PCR primer for mut
c 38		12.4	62.0	38	20	AAZ11115	PCR primer for E.c
c 39		12.4	62.0	38	21	AAA71224	Human KGF-2 E. col
c 40		12.4	62.0	38	22	AAF31922	PCR primer #1 for
c 41		12.4	62.0	48	24	ABN71862	Streptococcus agal
42		12.2	61.0	18	21	AAA38363	Human Ets-2 phosph
43		12.2	61.0	19	18	AAT91048	Prostate specific
44		12.2	61.0	19	20	AAX99838	PCR primer for pro
c 45		12.2	61.0	20	20	AAX87283	PRO344 forward PCR

ALIGNMENTS

RESULT 1
AAZ56186
ID AAZ56186 standard; DNA; 20 BP.
XX
AC AAZ56186;
XX
DT 28-MAR-2000 (first entry)
XX
DE Antisense oligonucleotide OD2 for inhibiting IL-4 receptor expression.
XX
KW Interleukin-4; IL-4; antisense oligonucleotide; asthma; allergy; cancer;
KW receptor expression inhibitor; immunoglobulin E; IgE; inflammation;
KW hypereosinophilia; ss.
XX
OS Homo sapiens.
XX
PN WO9966037-A2.
XX
PD 23-DEC-1999.
XX
PF 17-JUN-1999; 99WO-CA00572.
XX
PR 17-JUN-1998; 98CA-2235420.
XX
PA (REEX-) RECH EXPERTISES & DEV MEDICAUX PARENZ IN.
XX
PI Renzi P;
XX
DR WPI; 2000-097743/08.
XX
PT Antisense oligonucleotides directed to CCR3, interleukin or granulocyte
PT macrophage colony stimulating factor receptors, used for treating or

PT preventing asthma, allergies, hypereosinophilia, inflammation or cancer
PT -
XX
PS Claim 5; Page 17; 72pp; English.
XX
CC This is an antisense oligonucleotide directed against the interleukin-4
CC (IL-4) receptor, for inhibiting receptor expression. IL-4 is involved in
CC immunoglobulin E (IgE) production, the development and persistence of
CC asthma and atopy. The invention relates to antisense oligonucleotides
CC directed against a nucleic acid sequence encoding either a chemokine
CC receptor (CCR3), a common subunit of interleukin-4 (IL-4) and
CC interleukin-13 (IL-13) receptors, or a common subunit of interleukin-3
CC (IL-3), interleukin-5 (IL-5) and granulocyte macrophage colony
CC stimulating factor (GM-CSF) receptors. The antisense oligonucleotides can
CC be used in the treatment or prevention of asthma, allergy,
CC hypereosinophilia, general inflammation or cancer.
XX
SQ Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCCCAGAGCTTGCCACCT 20
||||||||||||||||||||
Db 1 GTTCCCAGAGCTTGCCACCT 20

RESULT 2
AAC73582/c
ID AAC73582 standard; DNA; 17 BP.
XX
AC AAC73582;
XX
DT 02-FEB-2001 (first entry)
XX
DE Reverse primer #128 used in multiplexing PCR/SBE assay.
XX
KW Oligonucleotide array; genotyping; single base extension reaction; SBE;
KW PCR primer; polymorphic locus; single nucleotide polymorphism; ss.
XX
OS Unidentified.
XX
PN WO200058516-A2.
XX
PD 05-OCT-2000.
XX
PF 27-MAR-2000; 2000WO-US08069.
XX
PR 26-MAR-1999; 99US-0126473.
PR 23-JUN-1999; 99US-0140359.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
PI Ryder T, Sklar P;
XX
DR WPI; 2000-656171/63.
XX
PT Universal array of oligonucleotides tags attached to a solid substrate
PT along with locus-specific tagged oligonucleotides useful in genotyping
PT using single base extension reactions -
XX
PS Example 7; Page 62; 83pp; English.
XX
CC The present invention relates to an oligonucleotide array comprising
CC oligonucleotide tags fixed to a solid substrate. The oligonucleotide
CC array is useful for genotyping a nucleic acid sample at one or more loci
CC via single base extension (SBE) reactions. A pair of primers is used to
CC amplify a polymorphic locus in a sample e.g. a single nucleotide
CC polymorphism (SNP). The present sequence is one of the primers used in
CC the method of the present invention to amplify a polymorphic sample. The
CC amplified nucleic acid product is then used as a template in a SBE
CC reaction with an extension primer. The SBE reaction products are used to
CC form the oligonucleotide array.
XX
SQ Sequence 17 BP; 4 A; 3 C; 7 G; 3 T; 0 other;

Query Match 69.0%; Score 13.8; DB 21; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCCAGAGCTTGCCACCT 20
|||||| ||||||| ||
Db 17 CCCAGATCTTGCCAGCT 1

RESULT 3
AAI67449
ID AAI67449 standard; DNA; 25 BP.
XX
AC AAI67449;
XX
DT 11-FEB-2002 (first entry)
XX
DE Probe sequence used for real-time RT-PCR analysis.
XX
KW ARP; angiogenesis; vascular endothelial growth factor; VEGF; cytostatic;
KW arginine-rich protein; cardiant; antirheumatic; antiarthritic; human;
KW antiatherosclerotic; vasotropic; gynecological; antidiabetic; vulnerary;
KW antiulcer; dermatological; ophthalmological; antipsoriatic; apoptosis;
KW gene therapy; RT-PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200170174-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09043.
XX
PR 21-MAR-2000; 2000US-191201P.
XX
PA (CURA-) CURAGEN CORP.
PA (GETH) GENENTECH INC.
XX
PI Rastelli LK, Gerber H;
XX
DR WPI; 2001-639087/73.
XX
PT Modulating angiogenesis and/or apoptosis for preventing or treating
PT cancer, myocardial infarction and promoting healing, by modulating the
PT activity of vascular endothelial growth factor-modulated gene
PT polypeptide -
XX
PS Example 2; Page 103; 155pp; English.
XX
CC The invention relates to modulating angiogenesis and cell survival that
CC involves modulating the activity of at least one vascular endothelial
CC growth factor (VEGF)-modulated gene polypeptide. The method is useful for
CC modulating angiogenesis and cell survival, for treating tumour and cancer
CC by decreasing angiogenesis in cancerous tumours and treating myocardial
CC infarction and promoting healing, by increasing angiogenesis. Transgenic
CC non-human animals, having disrupted arginine-rich protein (ARP), are
CC useful for determining the clinical stage of ovarian tumorous, which is
CC useful for determining if the tumour has potential for metastasis. ARP is
CC useful in gene therapy and in diagnostic applications. VEGFmg proteins
CC are useful in the treatment of tumours, neoplasias, hemangiomas,
CC rheumatoid arthritis, atherosclerosis, idiopathic pulmonary fibrosis,
CC vascular restenosis, arteriovenous malformations, meningioma, neovascular
CC glaucoma, psoriasis, hemophilic joints, hypertrophic scars, Osler-Weber
CC syndrome, scleroderma, vascular adhesion pathologies, synovitis,
CC dermatitis, endometriosis, diabetic retinopathy, neovascularization
CC associated with corneal injury or grafts, wound, sore, and ulcer healing.
CC Sequences AAI67449-487 represent probe primer sets used for real-time

```
CC   RT-PCR analysis of differential gene expression.
XX
SQ   Sequence 25 BP; 6 A; 7 C; 6 G; 6 T; 0 other;

  Query Match             68.0%;  Score 13.6;  DB 22;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCCACCT 20
           ||||||| || |||||  ||
Db       4 GTTCCCAAAGTTTGCCGGCT 23


RESULT 4
AAH22292
ID   AAH22292 standard; DNA; 25 BP.
XX
AC   AAH22292;
XX
DT   21-AUG-2001  (first entry)
XX
DE   Tissue factor pathway inhibitor-2 hybridisation probe SEQ ID NO:38.
XX
KW   Human; differentially expressed gene; angiogenesis; diagnosis;
KW   angiogenic disorder; wound healing; cancer; cardiovascular; psoriasis;
KW   vascular tumour; proliferative tumour; proliferative vitreoretinopathy;
KW   rheumatoid arthritis; Crohn's disease; atherosclerosis; endometriosis;
KW   neovascularisation; restenosis; hypertension; aneurysm; angina;
KW   myocardial infarction; chronic heart condition; osteoporosis;
KW   PCR primer; hybridisation; probe; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200132926-A2.
XX
PD   10-MAY-2001.
XX
PF   01-NOV-2000; 2000WO-US30051.
XX
PR   01-NOV-1999;   99US-0162699.
PR   13-APR-2000; 2000US-0196802.
PR   31-OCT-2000; 2000US-0703350.
XX
PA   (CURA-) CURAGEN CORP.
PA   (GETH ) GENENTECH INC.
XX
PI   Mehraban F,  Gerritsen M,  Rastelli L;
XX
DR   WPI; 2001-291056/30.
XX
PT   Differentially expressed genes involved in angiogenesis, useful for
PT   treating e.g. vascular tumors, atherosclerosis and/or restenosis
PT   subsequent to balloon angioplasty -
XX
PS   Example 19; Page 148; 182pp; English.
XX
CC   The present invention describes differentially expressed genes involved
CC   in angiogenesis (I), and the polypeptides that encode them. (I) have
CC   cardiovascular activity, and can be used in the modulation of
CC   angiogenesis. The nucleic acids and polypeptides may be used in the
CC   prevention, diagnosis and treatment of diseases associated with
CC   inappropriate angiogenesis. The polypeptides may also be used as antigens
CC   in the production of antibodies against them and in assays to identify
CC   modulators of their expression and activity. The antibodies and
CC   antagonists may also be used to down regulate expression and activity
CC   and modulate angiogenesis. The antibodies may also be used as diagnostic
CC   agents for detecting the presence of the polypeptides in samples.
CC   Disorders that may be prevented, diagnosed and/or treated by the above
CC   methods include, for example vascular tumours, proliferative tumours,
CC   proliferative vitreoretinopathy, rheumatoid arthritis, Crohn's disease,
CC   atherosclerosis, ovarian hyperstimulation, psoriasis, endometriosis
CC   associated with neovascularisation, restenosis subsequent to balloon
CC   angioplasty, scar tissue over production. peripheral vascular disease,
CC   hypertension, inflammatory vasculitides, Reynaud's disease and
CC   Reynaud's phenomenon, aneurysms, arterial restenosis, thrombophlebitis,
CC   lymphangitis, lymphedema, wound healing and tissue repair, ischaemia
CC   reperfusion injury, angina, myocardial infarctions, chronic heart
CC   conditions, heart failure such as congestive heart failure, age-related
CC   macular degeneration and osteoporosis. AAH22255 to AAH22325 and AAB98322
CC   to AAB98325 represent sequence used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 25 BP; 6 A; 7 C; 6 G; 6 T; 0 other;

  Query Match             68.0%;  Score 13.6;  DB 22;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCCACCT 20
           ||||||| || |||||  ||
Db       4 GTTCCCAAAGTTTGCCGGCT 23


RESULT 5
AAV95349
ID   AAV95349 standard; RNA; 17 BP.
XX
AC   AAV95349;
XX
DT   24-FEB-1999  (first entry)
XX
DE   Human c-fos target sequence nucleotide position 845.
XX
KW   Human; c-fos; hammerhead ribozyme; hairpin ribozyme; target site;
KW   cancer; oncogene; leukaemia; neuroblastoma; diagnosis; genetic drift;
KW   mutation; diseased cell; ss.
XX
OS   Homo sapiens.
XX
PN   WO9832846-A2.
XX
PD   30-JUL-1998.
XX
PF   20-JAN-1998;   98WO-US01017.
XX
PR   23-JAN-1997;   97US-0037658.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Jarvis T,  McSwiggen JA,  Stinchcomb DT;
XX
DR   WPI; 1998-427942/36.
XX
PT   Enzymatic nucleic acid molecules which specifically cleave RNA
PT   derived from a c-fos gene - useful for treating conditions related
PT   to levels of c-fos, especially cancer
XX
PS   Claim 2; Page 51; 72pp; English.
XX
CC   The present invention describes an enzymatic nucleic acid molecule which
CC   specifically cleaves RNA derived from a c-fos gene. AAV95401 to AAV95540
CC   and AAV95541 to AAV95584 represent hammerhead ribozymes and hairpin
CC   ribozymes, respectively, which specifically cleave human c-fos. AAV95261
CC   to AAV95400 and AAV95585 to AAV95628 represent human c-fos target
CC   sequences. The enzymatic nucleic acid molecules can be used for treating
CC   cancer associated with elevated levels of c-fos oncogene, especially
CC   leukaemias, neuroblastomas and lung, breast and colon cancers. The
CC   ribozymes may also be used as diagnostic tools to examine genetic drift
CC   and mutations within diseased cells, or to detect the presence of c-fos
CC   RNA in a cell.
XX
SQ   Sequence 17 BP; 3 A; 8 C; 4 G; 2 U; 0 other;

  Query Match             67.0%;  Score 13.4;  DB 19;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+03;
```

```
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 CCAGAGCTTGCCACC 19
           |||||| ::|||||||
Db       1 CCAGAGGUUGCCACC 15


RESULT 6
AAC83618/c
ID   AAC83618 standard; DNA; 20 BP.
XX
AC   AAC83618;
XX
DT   27-FEB-2001  (first entry)
XX
DE   Human c-fos oligo DNA D3.
XX
KW   Human; c-fos; fluorescent probe; cytoplasmic.nucleic acid detection; ss.
XX
OS   Homo sapiens.
XX
PN   EP1052293-A1.
XX
PD   15-NOV-2000.
XX
PF   27-DEC-1999;   99EP-0126030.
XX
PR   12-MAY-1999;   99JP-0131838.
XX
PA   (MOLE-) LAB MOLECULAR BIOPHOTONICS.
XX
PI   Tsuji A,  Hirano M,  Koshimoto H,  Ishibashi K;
XX
DR   WPI; 2001-018062/03.
XX
PT   Detection of a target nucleic acid in the cytoplasm of a living cell
PT   comprises using a fluorescent probe linked to a component that cannot
PT   permeate through the nuclear membrane  -
XX
PS   Example 1; Page 11; 53pp; English.
XX
CC   The present sequence is a probe which was used in a method for nucleic
CC   acid detection in cytoplasm. The method comprises detecting a target
CC   nucleic acid using a fluorescent hybridisation probe linked to a
CC   component that cannot permeate through the nuclear membrane of the
CC   cell. The present sequence was used for detecting cytoplasmic human
CC   c-fos mRNA molecules. The detection probe of this method is not
CC   readily degraded by endogenous cytoplasmic nucleases unlike currently
CC   available detection probes, as it has a specified structure which does
CC   not rapidly move to the nucleus when introduced into the cytoplasm of a
CC   living cell.
XX
SQ   Sequence 20 BP; 2 A; 6 C; 8 G; 4 T; 0 other;

  Query Match             67.0%;  Score 13.4;  DB 22;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 CCAGAGCTTGCCACC 19
           |||||| ||||||||
Db      20 CCAGAGGTTGCCACC 6


RESULT 7
AAC83624/c
ID   AAC83624 standard; DNA; 20 BP.
XX
AC   AAC83624;
XX
DT   27-FEB-2001  (first entry)
XX
DE   Human c-fos Bodipy493/503-labelled oligo DNA D3F.
XX
KW   Human; c-fos; fluorescent probe; cytoplasmic nucleic acid detection; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "attached to fluorescent dye Bodipy493/503"
XX
PN   EP1052293-A1.
XX
PD   15-NOV-2000.
XX
PF   27-DEC-1999;   99EP-0126030.
XX
PR   12-MAY-1999;   99JP-0131838.
XX
PA   (MOLE-) LAB MOLECULAR BIOPHOTONICS.
XX
PI   Tsuji A,  Hirano M,  Koshimoto H,  Ishibashi K;
XX
DR   WPI; 2001-018062/03.
XX
PT   Detection of a target nucleic acid in the cytoplasm of a living cell
PT   comprises using a fluorescent probe linked to a component that cannot
PT   permeate through the nuclear membrane  -
XX
PS   Example 1; Page 13; 53pp; English.
XX
CC   The present sequence is a probe which was used in a method for nucleic
CC   acid detection in cytoplasm. The method comprises detecting a target
CC   nucleic acid using a fluorescent hybridisation probe linked to a
CC   component that cannot permeate through the nuclear membrane of the
CC   cell. The present sequence was used for detecting cytoplasmic human
CC   c-fos mRNA molecules. The detection probe of this method is not
CC   readily degraded by endogenous cytoplasmic nucleases unlike currently
CC   available detection probes, as it has a specified structure which does
CC   not rapidly move to the nucleus when introduced into the cytoplasm of a
CC   living cell.
XX
SQ   Sequence 20 BP; 2 A; 6 C; 8 G; 4 T; 0 other;

  Query Match             67.0%;  Score 13.4;  DB 22;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 CCAGAGCTTGCCACC 19
           |||||| ||||||||
Db      20 CCAGAGGTTGCCACC 6


RESULT 8
ABI95431
ID   ABI95431 standard; DNA; 20 BP.
XX
AC   ABI95431;
XX
DT   16-FEB-2002  (first entry)
XX
DE   Capture oligonucleptide Zip ID#2518 oligo #9.
XX
KW   Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW   ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW   infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW   cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW   environmental monitoring; food industry; feed industry; ss.
XX
OS   Synthetic.
XX
PN   WO200179548-A2.
XX
PD   25-OCT-2001.
```

XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 29; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC medinesis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 other;

Query Match 66.0%; Score 13.2; DB 24; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TCCCAGAGCTTGCCACCT 20
|||| || ||||||| ||
Db 1 TCCCGGACCTTGCCATCT 18

RESULT 9
ABI87432
ID ABI87432 standard; DNA; 24 BP.
XX
AC ABI87432;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#2518 oligo #1.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.

XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 25; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC medinesis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 24 BP; 4 A; 10 C; 4 G; 6 T; 0 other;

Query Match 66.0%; Score 13.2; DB 24; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TCCCAGAGCTTGCCACCT 20
|||| || ||||||| ||
Db 1 TCCCGGACCTTGCCATCT 18

RESULT 10
ABI87433/c
ID ABI87433 standard; DNA; 24 BP.
XX
AC ABI87433;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#2518 oligo #2.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.

XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 25; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC medinesis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 24 BP; 6 A; 4 C; 10 G; 4 T; 0 other;

Query Match 66.0%; Score 13.2; DB 24; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TCCCAGAGCTTGCCACCT 20
|||| || ||||||| ||
Db 24 TCCCGGACCTTGCCATCT 7

RESULT 11
ABI88068
ID ABI88068 standard; DNA; 24 BP.
XX
AC ABI88068;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#2836 oligo #1.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.

XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 25; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC medinesis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 24 BP; 5 A; 7 C; 6 G; 6 T; 0 other;

Query Match 66.0%; Score 13.2; DB 24; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TCCCAGAGCTTGCCACCT 20
||||| |||||| || ||
Db 5 TCCCAAAGCTTGGCAACT 22

RESULT 12
ABI88069/c
ID ABI88069 standard; DNA; 24 BP.
XX
AC ABI88069;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#2836 oligo #2.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.

XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 25; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC medinesis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 24 BP; 6 A; 6 C; 7 G; 5 T; 0 other;

Query Match 66.0%; Score 13.2; DB 24; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TCCCAGAGCTTGCCACCT 20
||||| |||||| || ||
Db 20 TCCCAAAGCTTGGCAACT 3

RESULT 13
AAN91567
ID AAN91567 standard; DNA; 28 BP.
XX
AC AAN91567;
XX
DT 02-MAR-1990 (first entry)
XX
DE Neisseria gonorrhoea group 17 probe DNA.
XX
KW Escherichia coli; probe.
XX
OS Neisseria gonorrhoea.
XX
PN EP337896-A.
XX
PD 18-OCT-1989.
XX
PF 14-APR-1989; 89EP-0401045.
XX
PR 15-APR-1988; 88EP-0400929.
XX
PA (INNO) INNOGENETICS NV SA.
XX
PI Rossau R, Van Heuverswijn;
XX
DR WPI; 1989-302611/42.
XX
PT Hybridisation probes for detecting Neisseria strains
PT - some being specific for Neisseria gonorrhoeae
XX
PS Claim 1; page 27; 60pp; English.
XX
CC This probe, its complementary RNA, or its derivs. can be used to
CC specifically detect N. gonorrhoea, and can differentiate at the
CC sub-species level (eliminating Southern blotting).
XX
SQ Sequence 28 BP; 10 A; 9 C; 3 G; 6 T; 0 other;

Query Match 66.0%; Score 13.2; DB 10; Length 28;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTCCCAGAGCTTGCCACC 19
|||| | |||||||||| |
Db 7 TTCCAACAGCTTGCCAAC 24

RESULT 14
AAN91568
ID AAN91568 standard; RNA; 28 BP.
XX
AC AAN91568;
XX
DT 02-MAR-1990 (first entry)
XX
DE Neisseria gonorrhoea 17bis probe RNA.
XX
KW Escherichia coli; probe.
XX
OS Neisseria gonorrhoea.
XX
PN EP337896-A.
XX
PD 18-OCT-1989.
XX
PF 14-APR-1989; 89EP-0401045.
XX
PR 15-APR-1988; 88EP-0400929.
XX
PA (INNO) INNOGENETICS NV SA.
XX
PI Rossau R, Van Heuverswijn;
XX
DR WPI; 1989-302611/42.
XX
PT Hybridisation probes for detecting Neisseria strains
PT - some being specific for Neisseria gonorrhoeae
XX
PS Claim 1; page 28; 60pp; English.
XX
CC This probe, its complementary DNA, or its derivs. can be used to
CC specifically detect N. gonorrhoea, and can differentiate at the
CC sub-species level (eliminating Southern blotting).
XX
SQ Sequence 28 BP; 10 A; 9 C; 3 G; 6 U; 0 other;

Query Match 66.0%; Score 13.2; DB 10; Length 28;
Best Local Similarity 61.1%; Pred. No. 3.5e+03;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTCCCAGAGCTTGCCACC 19
::|| | |||::|||| |
Db 7 UUCCAACAGCUUGCCAAC 24

```
RESULT 15
AAN91569/c
ID   AAN91569 standard; DNA; 28 BP.
XX
AC   AAN91569;
XX
DT   02-MAR-1990  (first entry)
XX
DE   Neisseria gonorrhoea 17ter probe DNA.
XX
KW   Escherichia coli; probe.
XX
OS   Neisseria gonorrhoea.
XX
PN   EP337896-A.
XX
PD   18-OCT-1989.
XX
PF   14-APR-1989;   89EP-0401045.
XX
PR   15-APR-1988;   88EP-0400929.
XX
PA   (INNO ) INNOGENETICS NV SA.
XX
PI   Rossau R,  Van Heuverswijn;
XX
DR   WPI; 1989-302611/42.
XX
PT   Hybridisation probes for detecting Neisseria strains
PT   - some being specific for Neisseria gonorrhoeae
XX
PS   Claim 1; page 28; 60pp; English.
XX
CC   This probe, its complementary RNA, or its derivs. can be used to
CC   specifically detect N. gonorrhoea, and can differentiate at the
CC   sub-species level (eliminating Southern blotting).
XX
SQ   Sequence 28 BP; 6 A; 3 C; 9 G; 10 T; 0 other;

  Query Match             66.0%;  Score 13.2;  DB 10;  Length 28;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 TTCCCAGAGCTTGCCACC 19
           |||| | ||||||||| |
Db      22 TTCCAACAGCTTGCCAAC 5


Search completed: November 28, 2002, 17:24:11
Job time : 186.851 secs
```

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 16:42:34 ; Search time 1162.07 Seconds
(without alignments)
500.879 Million cell updates/sec

Title: US-09-719-737-2
Perfect score: 20
Sequence: 1 gttcccagagcttgccacct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20	100.0	20	6	AX008649	AX008649 Sequence
2	c	13.4	67.0	20	6	AR149434	AR149434 Sequence
3	c	13.4	67.0	20	6	AR149440	AR149440 Sequence
4	c	13.4	67.0	20	6	E49406	E49406 Method for
5	c	13.4	67.0	20	6	E49412	E49412 Method for
6		13.2	66.0	20	6	AX295389	AX295389 Sequence
7		13.2	66.0	24	6	AX290756	AX290756 Sequence
8		13.2	66.0	24	6	AX291074	AX291074 Sequence
9		13.2	66.0	28	6	A14537	A14537 Group 17 hy
10		13.2	66.0	28	6	A14538	A14538 Group 17 bi
11	c	13.2	66.0	28	6	A14539	A14539 Group 17 te
12	c	13.2	66.0	28	6	A14540	A14540 Group 17 qu
13		13.2	66.0	31	6	AX248913	AX248913 Sequence
14		13	65.0	35	6	AR212154	AR212154 Sequence
15		12.8	64.0	24	6	AX370542	AX370542 Sequence
16		12.8	64.0	26	6	AX453540	AX453540 Sequence
17	c	12.8	64.0	50	6	AX161154	AX161154 Sequence
18		12.6	63.0	20	6	AX412207	AX412207 Sequence
19	c	12.6	63.0	25	6	AX067206	AX067206 Sequence
20		12.6	63.0	29	6	A47119	A47119 Sequence 12
21	c	12.4	62.0	32	6	AX281557	AX281557 Sequence
22	c	12.4	62.0	32	6	AX281565	AX281565 Sequence
23	c	12.4	62.0	38	6	AR099158	AR099158 Sequence
24		12.2	61.0	19	6	I67855	I67855 Sequence 5
25		12.2	61.0	21	6	AX096742	AX096742 Sequence
26		12.2	61.0	21	6	E23807	E23807 Method for
27		12.2	61.0	24	6	I65283	I65283 Sequence 5
28		12.2	61.0	25	6	E06786	E06786 Primer. 9/1
29	c	12.2	61.0	27	6	AX455026	AX455026 Sequence
30		12.2	61.0	28	6	AR122021	AR122021 Sequence
31		12.2	61.0	28	6	AR173104	AR173104 Sequence
32		12.2	61.0	28	6	AX323159	AX323159 Sequence
33		12.2	61.0	31	6	AX425940	AX425940 Sequence
34	c	12.2	61.0	33	6	AR029549	AR029549 Sequence
35	c	12.2	61.0	33	6	AR098502	AR098502 Sequence
36	c	12.2	61.0	33	6	AX441428	AX441428 Sequence
37	c	12.2	61.0	33	6	AX453924	AX453924 Sequence
38	c	12.2	61.0	33	6	I41462	I41462 Sequence 59
39		12	60.0	21	6	AX096363	AX096363 Sequence
40		12	60.0	26	6	AX090084	AX090084 Sequence
41	c	12	60.0	27	6	I39768	I39768 Sequence 41
42		12	60.0	31	6	BD002915	BD002915 Gene comp
43		12	60.0	33	6	AX004493	AX004493 Sequence
44		12	60.0	40	6	AX138897	AX138897 Sequence
45		12	60.0	40	6	BD000662	BD000662 Growth ho

ALIGNMENTS

RESULT 1
AX008649
LOCUS AX008649 20 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 2 from Patent WO9966037.
ACCESSION AX008649
VERSION AX008649.1 GI:9996173
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Renzi,P.
TITLE Antisense oligonucleotides for treating or preventing atopic diseases and neoplastic cell proliferation
JOURNAL Patent: WO 9966037-A 2 23-DEC-1999;

```
          RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide inhibiting the common
                     subunit of IL-4 and IL-13 human receptor"
BASE COUNT        3 a      8 c      4 g      5 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCCACCT 20
           ||||||||||||||||||||
Db       1 GTTCCCAGAGCTTGCCACCT 20


RESULT 2
AR149434/c
LOCUS       AR149434                 20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 5 from patent US 6228592.
ACCESSION   AR149434
VERSION     AR149434.1  GI:15114025
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tsuji,A., Hirano,M., Koshimoto,H. and Ishibashi,K.
  TITLE     Nucleic acid detection in cytoplasm
  JOURNAL   Patent: US 6228592-A 5 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        2 a      6 c      8 g      4 t
ORIGIN

  Query Match             67.0%;  Score 13.4;  DB 6;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 5e+04;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 CCAGAGCTTGCCACC 19
           ||||||| ||||||||
Db      20 CCAGAGGTTGCCACC 6


RESULT 3
AR149440/c
LOCUS       AR149440                 20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 11 from patent US 6228592.
ACCESSION   AR149440
VERSION     AR149440.1  GI:15114031
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tsuji,A., Hirano,M., Koshimoto,H. and Ishibashi,K.
  TITLE     Nucleic acid detection in cytoplasm
  JOURNAL   Patent: US 6228592-A 11 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        2 a      6 c      8 g      4 t
ORIGIN

  Query Match             67.0%;  Score 13.4;  DB 6;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 5e+04;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 CCAGAGCTTGCCACC 19
           ||||||| ||||||||
Db      20 CCAGAGGTTGCCACC 6


RESULT 4
E49406/c
LOCUS       E49406                   20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method for detecting cytoplasmic target nucleic acid in living
            cell.
ACCESSION   E49406
VERSION     E49406.1  GI:18629305
KEYWORDS    JP 2001025400-A/5.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tsuji,A., Hirano,M., Koshimoto,H. and Ishibashi,K.
  TITLE     Method for detecting cytoplasmic target nucleic acid in living cell
  JOURNAL   Patent: JP 2001025400-A 5 30-JAN-2001;
            BUNSHI BIO HOTONIKUSU KENKYUSHO
COMMENT     OS   Artificial Sequence
            PN   JP 2001025400-A/5
            PD   30-JAN-2001
            PF   28-DEC-1999 JP 1999373904
            PR
            PI   AKIHIKO TSUJI,MASAHIKO HIRANO,HIROYUKI KOSHIMOTO, PI   KANAME
            ISHIBASHI
            PC   C12Q1/68,C12N15/09//G01N21/78,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        2 a      6 c      8 g      4 t
ORIGIN

  Query Match             67.0%;  Score 13.4;  DB 6;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 5e+04;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 CCAGAGCTTGCCACC 19
           ||||||| ||||||||
Db      20 CCAGAGGTTGCCACC 6


RESULT 5
E49412/c
LOCUS       E49412                   20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method for detecting cytoplasmic target nucleic acid in living
            cell.
ACCESSION   E49412
VERSION     E49412.1  GI:18629311
KEYWORDS    JP 2001025400-A/11.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tsuji,A., Hirano,M., Koshimoto,H. and Ishibashi,K.
  TITLE     Method for detecting cytoplasmic target nucleic acid in living cell
  JOURNAL   Patent: JP 2001025400-A 11 30-JAN-2001;
            BUNSHI BIO HOTONIKUSU KENKYUSHO
COMMENT     OS   Artificial Sequence
            PN   JP 2001025400-A/11
            PD   30-JAN-2001
            PF   28-DEC-1999 JP 1999373904
            PR
            PI   AKIHIKO TSUJI,MASAHIKO HIRANO,HIROYUKI KOSHIMOTO, PI   KANAME
            ISHIBASHI
            PC   C12Q1/68,C12N15/09//G01N21/78,C12N15/00
            CC
```

```
          FH   Key             Location/Qualifiers
          FT   source          1. .20
          FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        2 a      6 c      8 g      4 t
ORIGIN

  Query Match             67.0%;  Score 13.4;  DB 6;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 5e+04;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 CCAGAGCTTGCCACC 19
           ||||||  ||||||||
Db      20 CCAGAGGTTGCCACC 6


RESULT 6
AX295389
LOCUS       AX295389                  20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 7151 from Patent WO0179548.
ACCESSION   AX295389
VERSION     AX295389.1  GI:17057078
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 7151 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"
BASE COUNT        3 a      9 c      3 g      5 t
ORIGIN

  Query Match             66.0%;  Score 13.2;  DB 6;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 6.4e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3 TCCCAGAGCTTGCCACCT 20
           ||||  ||  |||||||  ||
Db       1 TCCCGGACCTTGCCATCT 18


RESULT 7
AX290756
LOCUS       AX290756                  24 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 2518 from Patent WO0179548.
ACCESSION   AX290756
VERSION     AX290756.1  GI:17052439
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 2518 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"
BASE COUNT        4 a      10 c      4 g      6 t
ORIGIN

  Query Match             66.0%;  Score 13.2;  DB 6;  Length 24;
  Best Local Similarity   83.3%;  Pred. No. 6.3e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3 TCCCAGAGCTTGCCACCT 20
           ||||  ||  |||||||  ||
Db       1 TCCCGGACCTTGCCATCT 18


RESULT 8
AX291074
LOCUS       AX291074                  24 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 2836 from Patent WO0179548.
ACCESSION   AX291074
VERSION     AX291074.1  GI:17052757
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 2836 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"
BASE COUNT        5 a      7 c      6 g      6 t
ORIGIN

  Query Match             66.0%;  Score 13.2;  DB 6;  Length 24;
  Best Local Similarity   83.3%;  Pred. No. 6.3e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3 TCCCAGAGCTTGCCACCT 20
           |||||  ||||||  ||  ||
Db       5 TCCCAAAGCTTGGCAACT 22


RESULT 9
A14537
LOCUS       A14537                    28 bp    DNA     linear   PAT 29-SEP-1994
DEFINITION  Group 17 hybridization probe for detecting Neisseria strains.
ACCESSION   A14537
VERSION     A14537.1  GI:640858
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Rossau,R. and Van Heuverswijn,H.
  TITLE     Hybridization probes for detecting neisseria strains
  JOURNAL   Patent: EP 0337896-A 68 18-OCT-1989;
            N.V. INNOGENETICS S.A
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT       10 a      9 c      3 g      6 t
ORIGIN

  Query Match             66.0%;  Score 13.2;  DB 6;  Length 28;
  Best Local Similarity   83.3%;  Pred. No. 6.3e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 TTCCCAGAGCTTGCCACC 19
           ||||  |  |||||||||  |
```

```
Db      7 TTCCAACAGCTTGCCAAC 24


RESULT 10
A14538
LOCUS       A14538                  28 bp    DNA     linear   PAT 29-SEP-1994
DEFINITION  Group 17 bis hybridization probe for detecting Neisseria strains.
ACCESSION   A14538
VERSION     A14538.1  GI:640859
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Rossau,R. and Van Heuverswijn,H.
  TITLE     Hybridization probes for detecting neisseria strains
  JOURNAL   Patent: EP 0337896-A 69 18-OCT-1989;
            N.V. INNOGENETICS S.A
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT       10 a      9 c      3 g      6 t
ORIGIN

  Query Match             66.0%;  Score 13.2;  DB 6;  Length 28;
  Best Local Similarity   83.3%;  Pred. No. 6.3e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 TTCCCAGAGCTTGCCACC 19
          |||| | ||||||||| |
Db      7 TTCCAACAGCTTGCCAAC 24


RESULT 11
A14539/c
LOCUS       A14539                  28 bp    DNA     linear   PAT 29-SEP-1994
DEFINITION  Group 17 ter hybridization probe for detecting Neisseria strains.
ACCESSION   A14539
VERSION     A14539.1  GI:640860
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Rossau,R. and Van Heuverswijn,H.
  TITLE     Hybridization probes for detecting neisseria strains
  JOURNAL   Patent: EP 0337896-A 70 18-OCT-1989;
            N.V. INNOGENETICS S.A
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        6 a      3 c      9 g     10 t
ORIGIN

  Query Match             66.0%;  Score 13.2;  DB 6;  Length 28;
  Best Local Similarity   83.3%;  Pred. No. 6.3e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 TTCCCAGAGCTTGCCACC 19
          |||| | ||||||||| |
Db     22 TTCCAACAGCTTGCCAAC 5


RESULT 12
A14540/c
LOCUS       A14540                  28 bp    DNA     linear   PAT 29-SEP-1994
DEFINITION  Group 17 quater hybridization probe for detecting Neisseria
            strains.
ACCESSION   A14540
VERSION     A14540.1  GI:640861
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Rossau,R. and Van Heuverswijn,H.
  TITLE     Hybridization probes for detecting neisseria strains
  JOURNAL   Patent: EP 0337896-A 71 18-OCT-1989;
            N.V. INNOGENETICS S.A
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        6 a      3 c      9 g     10 t
ORIGIN

  Query Match             66.0%;  Score 13.2;  DB 6;  Length 28;
  Best Local Similarity   83.3%;  Pred. No. 6.3e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 TTCCCAGAGCTTGCCACC 19
          |||| | ||||||||| |
Db     22 TTCCAACAGCTTGCCAAC 5


RESULT 13
AX248913
LOCUS       AX248913                31 bp    DNA     linear   PAT 28-SEP-2001
DEFINITION  Sequence 992 from Patent WO0166800.
ACCESSION   AX248913
VERSION     AX248913.1  GI:15863536
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Cargill,M., Ireland,J.S. and Lander,E.S.
  TITLE     Human single nucleotide polymorphisms
  JOURNAL   Patent: WO 0166800-A 992 13-SEP-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      14 c      7 g      7 t      1 others
ORIGIN

  Query Match             66.0%;  Score 13.2;  DB 6;  Length 31;
  Best Local Similarity   75.0%;  Pred. No. 6.2e+04;
  Matches   15;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 GTTCCCAGAGCTTGCCACCT 20
          ||||| :|||||   |||||
Db     10 GTTCCGRGAGCTGCTCACCT 29


RESULT 14
AR212154
LOCUS       AR212154                35 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 21 from patent US 6399571.
ACCESSION   AR212154
VERSION     AR212154.1  GI:21515663
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Gray,P.W. and Tjoelker,L.W.
  TITLE     Chitinase chitin-binding fragments
  JOURNAL   Patent: US 6399571-A 21 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="unknown"
```

```
BASE COUNT       13 a      8 c      6 g      8 t
ORIGIN

  Query Match             65.0%;  Score 13;  DB 6;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+04;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TTCCCAGAGCTTG 14
           |||||||||||||
Db       8 TTCCCAGAGCTTG 20


RESULT 15
AX370542
LOCUS       AX370542                 24 bp    DNA     linear   PAT 16-FEB-2002
DEFINITION  Sequence 61 from Patent WO0196371.
ACCESSION   AX370542
VERSION     AX370542.1  GI:18857578
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Broenner,G., Ciossek,T., Dohrmann,C., Haeder,T. and Rothe,M.
  TITLE     Adipose-related gene
  JOURNAL   Patent: WO 0196371-A 61 20-DEC-2001;
            DeveloGen AG (DE)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        7 a      9 c      6 g      2 t
ORIGIN

  Query Match             64.0%;  Score 12.8;  DB 6;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 1e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GTTCCCAGAGCTTGCC 16
           |||||||||||  |||
Db       3 GTTCCCAGAGCAGGCC 18


Search completed: November 28, 2002, 18:20:36
Job time : 1164.07 secs
```

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 17:10:34 ; Search time 1372.59 Seconds
(without alignments)
224.186 Million cell updates/sec

Title: US-09-719-737-9
Perfect score: 19
Sequence: 1 gggtctgcagcgggatggt 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	13.2	69.5	41	17	AZ619291	AZ619291 1M0451N02
c	2	13.2	69.5	43	9	AI036497	AI036497 ub65g12.r
c	3	13.2	69.5	50	9	AU107642	AU107642 AU107642
c	4	13.2	69.5	50	9	AU107643	AU107643 AU107643
c	5	12.6	66.3	43	17	AZ834659	AZ834659 2M0117B01
	6	12.4	65.3	50	9	AU105954	AU105954 AU105954
	7	12.2	64.2	38	12	BE736376	BE736376 601306513
	8	12.2	64.2	39	13	BI665248	BI665248 603288955
	9	12	63.2	39	12	BF788284	BF788284 602114017
c	10	12	63.2	43	9	AI197706	AI197706 ue48e12.r
c	11	12	63.2	50	9	AU107049	AU107049 AU107049
	12	11.8	62.1	46	9	AI188328	AI188328 qd13c07.x
c	13	11.8	62.1	48	17	AQ026239	AQ026239 1(3)L1170
c	14	11.8	62.1	50	9	AU107919	AU107919 AU107919
c	15	11.6	61.1	21	17	TA223G12Q	AL480787 T. brucei
	16	11.6	61.1	23	17	AZ351113	AZ351113 1M0088P19
	17	11.6	61.1	33	17	AZ972050	AZ972050 2M0245G14
	18	11.6	61.1	36	17	AZ581836	AZ581836 1M0370O13
	19	11.6	61.1	40	14	W66527	W66527 EST085 chic
c	20	11.6	61.1	40	14	W87969	W87969 mf65a02.r1
	21	11.6	61.1	46	17	AZ377453	AZ377453 1M0131M13
c	22	11.6	61.1	50	9	AU104493	AU104493 AU104493
c	23	11.4	60.0	40	9	AA711545	AA711545 vu24c05.r
c	24	11.4	60.0	43	10	AW247061	AW247061 2822604.5
c	25	11.4	60.0	45	17	TA388A10Q	AL498176 T. brucei
	26	11.4	60.0	50	9	AU103929	AU103929 AU103929
	27	11.2	58.9	38	9	AA108281	AA108281 EST0024 r
c	28	11.2	58.9	38	14	H51687	H51687 yp81h05.r1
c	29	11.2	58.9	45	17	BH643822	BH643822 1008060D0
c	30	11.2	58.9	46	17	BH803079	BH803079 1008098H1
	31	11.2	58.9	50	9	AU102320	AU102320 AU102320
c	32	11.2	58.9	50	9	AU103464	AU103464 AU103464
c	33	11.2	58.9	50	9	AU104693	AU104693 AU104693
c	34	11.2	58.9	50	9	AU104722	AU104722 AU104722
c	35	11.2	58.9	50	9	AU104725	AU104725 AU104725
c	36	11.2	58.9	50	9	AU104728	AU104728 AU104728
c	37	11	57.9	19	17	AZ510143	AZ510143 1M0354P21
	38	11	57.9	37	13	BI080927	BI080927 602878838
c	39	11	57.9	37	14	W73807	W73807 zd50h01.r1
	40	11	57.9	40	9	AA928933	AA928933 oo31b09.s
c	41	11	57.9	41	17	AZ842109	AZ842109 2M0140M22
	42	11	57.9	42	17	AZ818778	AZ818778 2M0089E06
	43	11	57.9	43	9	AA974942	AA974942 on34h12.s
	44	11	57.9	46	9	AA530925	AA530925 nj47a12.s
c	45	11	57.9	46	9	AA568369	AA568369 nl88c09.s

ALIGNMENTS

RESULT 1
AZ619291/c
LOCUS AZ619291 41 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0451N02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0451N02 F, DNA sequence.
ACCESSION AZ619291
VERSION AZ619291.1 GI:11741481
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 41)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

```
            Plate: 0451  row: N  column: 02
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 41.
FEATURES              Location/Qualifiers
     source           1. .41
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0451N02"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/).. The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|47321141|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT         8 a      20 c       8 g       5 t
ORIGIN

  Query Match             69.5%;  Score 13.2;  DB 17;  Length 41;
  Best Local Similarity   83.3%;  Pred. No. 5.5e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGG 18
           |||| ||||| ||| |||
Db      20 GGGTGTGCAGGGGGCTGG 3


RESULT 2
AI036497/c
LOCUS       AI036497                  43 bp    mRNA    linear   EST 26-JUN-1998
DEFINITION  ub65g12.r1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
            IMAGE:1382662 5' similar to SW:EMP2_HUMAN P54851 EPITHELIAL
            MEMBRANE PROTEIN-2 ;, mRNA sequence.
ACCESSION   AI036497
VERSION     AI036497.1  GI:3260188
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:905130
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .43
                      /organism="Mus musculus"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:1382662"
                      /clone_lib="Soares_mammary_gland_NMLMG"
                      /sex="female (lactating)"
                      /tissue_type="mammary gland"
                      /lab_host="DH10B"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; 1st strand cDNA was prepared from mammary
                      gland tissue from a lactating female, and was then primed
                      with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                      ligated to Eco RI adaptors (Pharmacia), digested with Not
                      I  and cloned into the Not I and Eco RI sites of the
                      modified pT7T3 vector.  Library is normalized.  Library
                      was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT         7 a      20 c       12 g       4 t
ORIGIN

  Query Match             69.5%;  Score 13.2;  DB 9;  Length 43;
  Best Local Similarity   83.3%;  Pred. No. 5.6e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 GGTCTGCAGCGGGATGGT 19
           |||| || | ||||||||
Db      26 GGTCGGCGGGGGGATGGT 9


RESULT 3
AU107642/c
LOCUS       AU107642                  50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU107642 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            LNG11936, mRNA sequence.
ACCESSION   AU107642
VERSION     AU107642.1  GI:13557163
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y:, Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES              Location/Qualifiers
     source           1. .50
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="LNG11936"
                      /clone_lib="Sugano Homo sapiens cDNA library"
                      /note="Differential display comparison of untreated and
                      dimethylfumarate treated U937 cells"
BASE COUNT         8 a      20 c       10 g       12 t
ORIGIN
```

```
  Query Match            69.5%;  Score 13.2;  DB 9;  Length 50;
  Best Local Similarity  83.3%;  Pred. No. 5.7e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGG 18
           ||| ||||| ||||| ||
Db      45 GGGACTGCATCGGGAAGG 28


RESULT 4
AU107643/c
LOCUS       AU107643                 50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU107643 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            ZRV6C769, mRNA sequence.
ACCESSION   AU107643
VERSION     AU107643.1  GI:13557164
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="ZRV6C769"
                     /clone_lib="Sugano Homo sapiens cDNA library"
                     /note="Differential display comparison of untreated and
                     dimethylfumarate treated U937 cells"
BASE COUNT        9 a     21 c     10 g     10 t
ORIGIN

  Query Match            69.5%;  Score 13.2;  DB 9;  Length 50;
  Best Local Similarity  83.3%;  Pred. No. 5.7e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGG 18
           ||| ||||| ||||| ||
Db      42 GGGACTGCATCGGGAAGG 25


RESULT 5
AZ834659/c
LOCUS       AZ834659                 43 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0117B01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0117B01 R, DNA sequence.
ACCESSION   AZ834659
VERSION     AZ834659.1  GI:13004567
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000  Std Error: 0.00
            Plate: 0117  row: B  column: 01
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 43.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0117B01"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        7 a     17 c      6 g     13 t
ORIGIN

  Query Match            66.3%;  Score 12.6;  DB 17;  Length 43;
  Best Local Similarity  78.9%;  Pred. No. 1e+05;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           | |  |||||||||| ||
Db      22 GAGGGTGCAGCGGGATTGT 4


RESULT 6
AU105954
LOCUS       AU105954                 50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU105954 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            INEB0085, mRNA sequence.
ACCESSION   AU105954
VERSION     AU105954.1  GI:13555475
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
```

```
          ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="INEB0085"
                     /clone_lib="Sugano Homo sapiens cDNA library"
                     /note="Differential display comparison of untreated and
                     dimethylfumarate treated U937 cells"
BASE COUNT       12 a      10 c      18 g      10 t
ORIGIN

  Query Match             65.3%;  Score 12.4;  DB 9;  Length 50;
  Best Local Similarity   92.9%;  Pred. No. 1.3e+05;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 GTCTGCAGCGGGAT 16
           ||||||||  |||||
Db      33 GTCTGCAGAGGGAT 46


RESULT 7
BE736376
LOCUS       BE736376                 38 bp    mRNA    linear   EST 15-SEP-2000
DEFINITION  601306513F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640802 5',
            mRNA sequence.
ACCESSION   BE736376
VERSION     BE736376.1  GI:10150368
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM345  row: j  column: 03
            High quality sequence stop: 38.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3640802"
                     /clone_lib="NIH_MGC_39"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Library constructed
                     by Ling Hong in the laboratory of Gerald M. Rubin
                     (University of California,  Berkeley) using ZAP-cDNA
                     synthesis kit (Stratagene) and Superscript II RT (Life
                     Technologies)."
BASE COUNT        9 a       6 c      19 g       4 t
ORIGIN

  Query Match             64.2%;  Score 12.2;  DB 12;  Length 38;
  Best Local Similarity   82.4%;  Pred. No. 1.5e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATG 17
           ||| ||||||| ||| |
Db       7 GGGCCTGCAGCTGGAGG 23


RESULT 8
BI665248
LOCUS       BI665248                 39 bp    mRNA    linear   EST 12-SEP-2001
DEFINITION  603288955F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5323189 5',
            mRNA sequence.
ACCESSION   BI665248
VERSION     BI665248.1  GI:15579481
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey Green M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11819  row: m  column: 14
            High quality sequence stop: 39.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5323189"
                     /clone_lib="NCI_CGAP_Mam6"
                     /sex="female, virgin"
                     /tissue_type="infiltrating ductal carcinoma"
                     /dev_stage="5 months"
                     /lab_host="DH10B"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT        8 a       9 c      13 g       9 t
ORIGIN

  Query Match             64.2%;  Score 12.2;  DB 13;  Length 39;
  Best Local Similarity   82.4%;  Pred. No. 1.5e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 GGTCTGCAGCGGGATGG 18
           | ||||||||| ||| ||
Db      19 GTTCTGCAGCTGGAAGG 35


RESULT 9
BF788284
LOCUS       BF788284                 39 bp    mRNA    linear   EST 12-JAN-2001
DEFINITION  602114017F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4241957
```

```
            5', mRNA sequence.
ACCESSION   BF788284
VERSION     BF788284.1  GI:12093320
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9859  row: b  column: 06
            High quality sequence stop: 39.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4241957"
                     /clone_lib="NCI_CGAP_Kid14"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT        7 a     10 c     15 g      7 t
ORIGIN

  Query Match             63.2%;  Score 12;  DB 12;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+05;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 TGCAGCGGGATG 17
           ||||||||||||
Db       9 TGCAGCGGGATG 20


RESULT 10
AI197706/c
LOCUS       AI197706                  43 bp    mRNA    linear   EST 14-OCT-1998
DEFINITION  ue48e12.r1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
            IMAGE:1494382 5' similar to TR:O16786 O16786 T21D12.3 PROTEIN. ;,
            mRNA sequence.
ACCESSION   AI197706
VERSION     AI197706.1  GI:3750312
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:931986
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1494382"
                     /clone_lib="Soares_mammary_gland_NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT        5 a     14 c     16 g      8 t
ORIGIN

  Query Match             63.2%;  Score 12;  DB 9;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+05;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCG 12
           ||||||||||||
Db      26 GGGTCTGCAGCG 15


RESULT 11
AU107049/c
LOCUS       AU107049                  50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU107049 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            KAT03213, mRNA sequence.
ACCESSION   AU107049
VERSION     AU107049.1  GI:13556570
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="KAT03213"
                     /clone_lib="Sugano Homo sapiens cDNA library"
                     /note="Differential display comparison of untreated and
```

```
                dimethylfumarate treated U937 cells"
BASE COUNT        9 a      14 c      22 g       5 t
ORIGIN

  Query Match             63.2%;  Score 12;  DB 9;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+05;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCG 12
           ||||||||||||
Db      49 GGGTCTGCAGCG 38


RESULT 12
AI188328
LOCUS       AI188328                 46 bp    mRNA    linear   EST 28-OCT-1998
DEFINITION  qd13c07.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:1723596 3' similar to SW:GA45_CRILO P24523 GROWTH
            ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD45. ;, mRNA sequence.
ACCESSION   AI188328
VERSION     AI188328.1  GI:3739537
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 1083   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1723596"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT       13 a      10 c      14 g       9 t
ORIGIN

  Query Match             62.1%;  Score 11.8;  DB 9;  Length 46;
  Best Local Similarity   86.7%;  Pred. No. 2.3e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGA 15
           || |||||||||  ||
Db      31 GGATCTGCAGCGCGA 45


RESULT 13
AQ026239/c
LOCUS       AQ026239                 48 bp    DNA     linear   GSS 30-JUN-1998
DEFINITION  l(3)L1170 Drosophila melanogaster P lethal line Drosophila
            melanogaster genomic Sequence recovered from 5' end of P element,
            DNA sequence.
ACCESSION   AQ026239
VERSION     AQ026239.1  GI:3266524
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Spradling,A.C., Stern,D., Beaton,A., Rehm,E.J., Laverty,T., Mozden
            ,N., Misra,S. and Rubin,G.M.
  TITLE     The BDGP gene disruption project: Single P element insertions
            mutating 30% of Drosophila autosomal genes
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Gerald Rubin
            Berkeley Drosophila Genome Project
            University of California, Berkeley
            LSA Building, Berkeley, CA 94720-3200, USA
            Fax: 5106439947
            Email: gerry@fruitfly.berkeley.edu
            Sequence recovery method was inverse PCR.

            Sequence orientation is forward strand relative to 5' end of P
            element

            The P element insertion position is base 041 in the 48 bases. This
            insertion position refers to the first base of the 8 base target
            recognition sequence.
            Class: transposon-tagged.
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="Drosophila melanogaster P lethal line"
                     /note="Inverse PCR was performed on Drosophila
                     melanogaster strains each of which contains a single P
                     transposable element insertion that is thought to cause
                     either lethality or sterility. The resultant fragment for
                     each strain was directly sequenced to determine the
                     genomic sequence at the site of insertion. Details of the
                     protocols used can be found at
                     http://fruitfly.berkeley.edu/p_disrupt/inverse_pcr.html."
BASE COUNT       15 a      13 c      18 g       2 t
ORIGIN

  Query Match             62.1%;  Score 11.8;  DB 17;  Length 48;
  Best Local Similarity   86.7%;  Pred. No. 2.3e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5 CTGCAGCGGGATGGT 19
           ||||||| | |||||
Db      48 CTGCAGCCGCATGGT 34


RESULT 14
AU107919/c
LOCUS       AU107919                 50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU107919 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            ZRV61844, mRNA sequence.
ACCESSION   AU107919
VERSION     AU107919.1  GI:13557441
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
```

mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano ,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES Location/Qualifiers
source 1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ZRV61844"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"
BASE COUNT 9 a 11 c 8 g 22 t
ORIGIN

Query Match 62.1%; Score 11.8; DB 9; Length 50;
Best Local Similarity 86.7%; Pred. No. 2.3e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTGCAGCGGGATGG 18
||||||| ||| ||
Db 20 TCTGCAGCTGGAGGG 6

RESULT 15
TA223G12Q/c
LOCUS TA223G12Q 21 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 223g12, reverse sequence, genomic survey sequence.
ACCESSION AL480787
VERSION AL480787.1 GI:11846556
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 21)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES Location/Qualifiers
source 1. .21
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="223g12"
BASE COUNT 5 a 8 c 5 g 3 t
ORIGIN

Query Match 61.1%; Score 11.6; DB 17; Length 21;
Best Local Similarity 77.8%; Pred. No. 2.4e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGTCTGCAGCGGGATGGT 19
||| ||| |||| || ||
Db 21 GGTATGCTGCGGCATCGT 4

Search completed: November 28, 2002, 19:30:44
Job time : 1375.59 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 17:15:39 ; Search time 39.9655 Seconds
(without alignments)
183.088 Million cell updates/sec

Title: US-09-719-737-9
Perfect score: 19
Sequence: 1 gggtctgcagcgggatggt 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 341543 seqs, 192557720 residues

Total number of hits satisfying chosen parameters: 177872

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	14.2	74.7	20	10	US-09-733-294A-63	Sequence 63, Appl
	2	13.2	69.5	38	10	US-09-349-954A-13	Sequence 13, Appl
	3	13.2	69.5	38	10	US-09-907-007-13	Sequence 13, Appl
c	4	12.6	66.3	30	10	US-09-730-716-11	Sequence 11, Appl
c	5	12.6	66.3	35	9	US-09-826-025-6	Sequence 6, Appli
c	6	12.6	66.3	38	10	US-09-850-165-61	Sequence 61, Appl
c	7	12.6	66.3	41	9	US-09-925-664-66	Sequence 66, Appl
c	8	12.6	66.3	43	10	US-09-766-378A-2	Sequence 2, Appli
c	9	12.6	66.3	44	10	US-09-848-164-40	Sequence 40, Appl
c	10	12.2	64.2	21	10	US-09-838-785-8	Sequence 8, Appli
c	11	12.2	64.2	31	10	US-09-801-274-1241	Sequence 1241, Ap
c	12	12	63.2	31	10	US-09-801-274-1005	Sequence 1005, Ap
c	13	12	63.2	31	10	US-09-801-274-1006	Sequence 1006, Ap
	14	11.8	62.1	20	8	US-08-591-486B-100	Sequence 100, App
	15	11.8	62.1	20	10	US-09-752-639-110	Sequence 110, App
	16	11.8	62.1	20	10	US-09-984-198-110	Sequence 110, App
	17	11.8	62.1	26	10	US-09-872-761-9	Sequence 9, Appli
c	18	11.6	61.1	20	10	US-09-838-785-17	Sequence 17, Appl
c	19	11.6	61.1	45	10	US-09-850-165-24	Sequence 24, Appl
	20	11.4	60.0	16	12	US-10-007-628-13	Sequence 13, Appl
	21	11.4	60.0	29	10	US-09-729-674-250	Sequence 250, App
	22	11.2	58.9	20	10	US-09-727-198-3	Sequence 3, Appli
c	23	11.2	58.9	24	10	US-09-947-770-34	Sequence 34, Appl
c	24	11.2	58.9	30	9	US-09-252-150-58	Sequence 58, Appl
c	25	11.2	58.9	31	10	US-09-801-274-1098	Sequence 1098, Ap
	26	11.2	58.9	31	10	US-09-801-274-1217	Sequence 1217, Ap
	27	11.2	58.9	36	10	US-09-896-852-34	Sequence 34, Appl
	28	11.2	58.9	36	12	US-10-020-139-7	Sequence 7, Appli
c	29	11.2	58.9	39	9	US-09-430-029-12	Sequence 12, Appl
c	30	11.2	58.9	40	9	US-10-113-246-3	Sequence 3, Appli
c	31	11.2	58.9	40	9	US-10-113-238-3	Sequence 3, Appli
c	32	11.2	58.9	40	10	US-09-896-852-32	Sequence 32, Appl
c	33	11.2	58.9	40	10	US-09-865-807-40	Sequence 40, Appl
c	34	11.2	58.9	40	10	US-09-944-604-7	Sequence 7, Appli
c	35	11.2	58.9	40	10	US-09-757-207-2	Sequence 2, Appli
c	36	11.2	58.9	40	10	US-09-757-207-5	Sequence 5, Appli
c	37	11.2	58.9	40	10	US-09-757-207-6	Sequence 6, Appli
c	38	11.2	58.9	41	10	US-09-757-207-1	Sequence 1, Appli
c	39	11.2	58.9	41	10	US-09-757-207-7	Sequence 7, Appli
c	40	11.2	58.9	42	10	US-09-778-168-12	Sequence 12, Appl
c	41	11.2	58.9	42	10	US-09-778-175-12	Sequence 12, Appl
c	42	11.2	58.9	42	10	US-09-335-218-12	Sequence 12, Appl
c	43	11.2	58.9	44	10	US-09-778-168-6	Sequence 6, Appli
c	44	11.2	58.9	44	10	US-09-778-175-6	Sequence 6, Appli
c	45	11.2	58.9	44	10	US-09-335-218-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-733-294A-63
; Sequence 63, Application US/09733294A
; Patent No. US20020045588A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wancewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-733-294A-63

Query Match 74.7%; Score 14.2; DB 10; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 GGGTCTGCAGCGGGATGGT 19
          |||||| || | |||||||
Db      1 GGGTCTCCACCTGGATGGT 19
```

RESULT 2
US-09-349-954A-13
; Sequence 13, Application US/09349954A
; Patent No. US20020019027A1
; GENERAL INFORMATION:
; APPLICANT: Hayward, Nicholas K.
; APPLICANT: Weber, Gunther
; APPLICANT: Grimmond, Sean
; APPLICANT: No. US20020019027A1denskjold, Magnus

```
;  APPLICANT:  Larsson, Catharina
;  TITLE OF INVENTION:  A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
;  TITLE OF INVENTION:  SAME
;  FILE REFERENCE:  Dav. Col. Cave
;  CURRENT APPLICATION NUMBER: US/09/349,954A
;  CURRENT FILING DATE:  1999-07-08
;  PRIOR APPLICATION NUMBER:  08/765,588
;  PRIOR FILING DATE:  1996-02-22
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 38
;   TYPE: DNA
;   ORGANISM: Oligonucleotide
US-09-349-954A-13

  Query Match             69.5%;  Score 13.2;  DB 10;  Length 38;
  Best Local Similarity   83.3%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGG 18
           ||| ||| || |||||||
Db       7 GGGGCTGGAGTGGGATGG 24


RESULT 3
US-09-907-007-13
; Sequence 13, Application US/09907007
; Patent No. US20020142395A1
; GENERAL INFORMATION:
;  APPLICANT: Hayward, Nicholas K.
;  APPLICANT:  Weber, Gunther
;  APPLICANT:  Grimmond, Sean
;  APPLICANT:  No. US20020142395Aldenskjold, Magnus
;  APPLICANT:  Larsson, Catharina
;  TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
;  TITLE OF INVENTION:  SAME
;  FILE REFERENCE: DAVIES
;  CURRENT APPLICATION NUMBER: US/09/907,007
;  CURRENT FILING DATE:  2001-07-17
;  PRIOR APPLICATION NUMBER: 08/765,588
;  PRIOR FILING DATE: 1996-02-22
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 38
;   TYPE: DNA
;   ORGANISM: Oligonucleotide
US-09-907-007-13

  Query Match             69.5%;  Score 13.2;  DB 10;  Length 38;
  Best Local Similarity   83.3%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGG 18
           ||| ||| || |||||||
Db       7 GGGGCTGGAGTGGGATGG 24


RESULT 4
US-09-730-716-11/c
; Sequence 11, Application US/09730716
; Patent No. US20010004531A1
; GENERAL INFORMATION:
;  APPLICANT:  Young Chul Sung
;  APPLICANT:  You Suk Suh
;  TITLE OF INVENTION:  AIDS DNA VACCINE THAT PREVENTS SIVmac239
;  TITLE OF INVENTION:  VIRUS INFECTION IN MONKEYS
;  FILE REFERENCE:  118.6-US-01
;  CURRENT APPLICATION NUMBER: US/09/730,716
;  CURRENT FILING DATE:  2000-12-06
;  PRIOR APPLICATION NUMBER:  KR 1999-55129
;  PRIOR FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS:  12
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: hGM-CSF specific primer (forward)
US-09-730-716-11

  Query Match             66.3%;  Score 12.6;  DB 10;  Length 30;
  Best Local Similarity   78.9%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           || ||||||||   |||||
Db      22 GGCTCTGCAGCCCCATGGT 4


RESULT 5
US-09-826-025-6/c
; Sequence 6, Application US/09826025
; Patent No. US20020162123A1
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Combination Immunogene Therapy
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Medlen & Carroll, LLP
;             STREET: 220 Montgomery Street, Suite 2200
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/826,025
;             FILING DATE: 04-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ingolia, Diane E.
;             REGISTRATION NUMBER: 40,027
;             REFERENCE/DOCKET NUMBER: CHANG-02687
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 705-8410
;             TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 35 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-826-025-6

  Query Match             66.3%;  Score 12.6;  DB 9;  Length 35;
  Best Local Similarity   78.9%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           || ||||||||   |||||
Db      33 GGCTCTGCAGCCACATGGT 15
```

```
RESULT 6
US-09-850-165-61/c
; Sequence 61, Application US/09850165
; Patent No. US20020150580A1
; GENERAL INFORMATION:
;  APPLICANT: NEWMAN, ROLAND A.
;  APPLICANT:  HANNA, NABIL
;  APPLICANT:  RAAB, RONALD W.
;  TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
;  FILE REFERENCE: 037003-0280614
;  CURRENT APPLICATION NUMBER: US/09/850,165
;  CURRENT FILING DATE:  2001-05-08
;  PRIOR APPLICATION NUMBER: 09/082,472
;  PRIOR FILING DATE: 1998-05-21
;  PRIOR APPLICATION NUMBER: 08/476,237
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 08/397,072
;  PRIOR FILING DATE: 1995-04-17
;  PRIOR APPLICATION NUMBER: 07/912,292
;  PRIOR FILING DATE: 1992-07-10
;  PRIOR APPLICATION NUMBER: 07/856,281
;  PRIOR FILING DATE: 1992-03-23
;  PRIOR APPLICATION NUMBER: 07/735,064
;  PRIOR FILING DATE: 1991-07-25
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
;   LENGTH: 38
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-850-165-61

  Query Match             66.3%;  Score 12.6;  DB 10;  Length 38;
  Best Local Similarity   78.9%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           ||||||||| |   |||||
Db      33 GGGTCTGCAACACCATGGT 15


RESULT 7
US-09-925-664-66/c
; Sequence 66, Application US/09925664
; Patent No. US20020160006A1
; GENERAL INFORMATION:
;  APPLICANT: Denney, Jr., Dan W.
;  TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
;  FILE REFERENCE: GENITOPE-06499
;  CURRENT APPLICATION NUMBER: US/09/925,664
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/370,453
;  PRIOR FILING DATE: 1999-08-09
;  PRIOR APPLICATION NUMBER: 08/644,664
;  PRIOR FILING DATE: 1996-05-01
;  PRIOR APPLICATION NUMBER: 08/761,277
;  PRIOR FILING DATE: 1996-12-06
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 41
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-925-664-66

  Query Match             66.3%;  Score 12.6;  DB 9;  Length 41;
  Best Local Similarity   78.9%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           ||||||||| |   |||||
Db      37 GGGTCTGCAACACCATGGT 19


RESULT 8
US-09-766-378A-2/c
; Sequence 2, Application US/09766378A
; Patent No. US20020091079A1
;   GENERAL INFORMATION:
;        APPLICANT: Rhode, Peter R.
;                   Acevedo, Jorge
;                   Burkhardt, Martin
;                   Jiao, Jin-an
;                   Wong, Hing C.
;        TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
;                            METHODS OF USE THEREOF
;        NUMBER OF SEQUENCES: 38
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
;             STREET: 130 Water Street
;             CITY: Boston
;             STATE: MA
;             COUNTRY: usa
;             ZIP: 02109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/766,378A
;             FILING DATE: 19-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/960,190
;             FILING DATE: 29-OCT-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Corless, Peter F
;             REGISTRATION NUMBER: 33,860
;             REFERENCE/DOCKET NUMBER: 48002-DIV
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 617-523-3400
;             TELEFAX: 617-523-6440
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 43 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-766-378A-2

  Query Match             66.3%;  Score 12.6;  DB 10;  Length 43;
  Best Local Similarity   78.9%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           || ||||||| |  |||||
Db      38 GGATCTGCAGAGCCATGGT 20


RESULT 9
US-09-848-164-40/c
; Sequence 40, Application US/09848164
; Patent No. US20020034513A1
;   GENERAL INFORMATION:
;        APPLICANT: Rhode, Peter R.
;                   Jiao, Jin-An
;                   Burkhardt, Martin
;                   Wong, Hing
;        TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
```

```
;       NUMBER OF SEQUENCES: 124
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Dade International, Inc.
;            STREET: 1717 Deerfield Road
;            CITY: Deerfield
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60015
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/848,164
;            FILING DATE: 03-May-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/067,615
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: US 08/382,454
;            FILING DATE: 01-FEB-1995
;            APPLICATION NUMBER: US 08/283,302
;            FILING DATE: 29-JUL-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Pearson, Louise S.
;            REGISTRATION NUMBER: 32,369
;            REFERENCE/DOCKET NUMBER: STR-4665-CIP2
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (708) 267-5300
;            TELEFAX: (708) 267-5376
;   INFORMATION FOR SEQ ID NO: 40:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 44 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: unknown
;            TOPOLOGY: unknown
;       SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-848-164-40

  Query Match             66.3%;  Score 12.6;  DB 10;  Length 44;
  Best Local Similarity   78.9%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           || ||||||| |  |||||
Db      39 GGATCTGCAGAGCCATGGT 21


RESULT 10
US-09-838-785-8/c
; Sequence 8, Application US/09838785
; Patent No. US20020009455A1
; GENERAL INFORMATION:
;  APPLICANT: Lau, Ted
;  APPLICANT:  Lin, Rick
;  APPLICANT:  Parkes, Debbie
;  APPLICANT:  Parry, Gordon
;  APPLICANT:  Schneider, Douglas
;  APPLICANT:  Steinbrecher, Renate
;  APPLICANT:  Van Heult, Pam T
;  APPLICANT:  Wu, John
;  TITLE OF INVENTION: DNA Encoding a No. US20020009455A1el PROST 03
;  FILE REFERENCE: 51831AUSM1
;  CURRENT APPLICATION NUMBER: US/09/838,785
;  CURRENT FILING DATE:  2001-04-20
;  PRIOR APPLICATION NUMBER: 60/200,065
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-838-785-8

  Query Match             64.2%;  Score 12.2;  DB 10;  Length 21;
  Best Local Similarity   82.4%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 GGTCTGCAGCGGGATGG 18
           | | |||||| ||||||
Db      17 GCTGTGCAGCTGGATGG 1


RESULT 11
US-09-801-274-1241/c
; Sequence 1241, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
;  APPLICANT: Cargill, Michele
;  APPLICANT:  Ireland, James S.
;  APPLICANT:  Lander, Eric S.
;  TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
;  FILE REFERENCE: 2825.2009-001
;  CURRENT APPLICATION NUMBER: US/09/801,274
;  CURRENT FILING DATE:  2001-03-07
;  PRIOR APPLICATION NUMBER: US 60/187,510
;  PRIOR FILING DATE: 2000-03-07
;  PRIOR APPLICATION NUMBER: US 60/206,129
;  PRIOR FILING DATE: 2000-05-22
;  NUMBER OF SEQ ID NOS: 1802
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1241
;   LENGTH: 31
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-801-274-1241

  Query Match             64.2%;  Score 12.2;  DB 10;  Length 31;
  Best Local Similarity   82.4%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 GGTCTGCAGCGGGATGG 18
           |||||| || ||| |||
Db      25 GGTCTGTAGRGGGGTGG 9


RESULT 12
US-09-801-274-1005/c
; Sequence 1005, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
;  APPLICANT: Cargill, Michele
;  APPLICANT:  Ireland, James S.
;  APPLICANT:  Lander, Eric S.
;  TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
;  FILE REFERENCE: 2825.2009-001
;  CURRENT APPLICATION NUMBER: US/09/801,274
;  CURRENT FILING DATE:  2001-03-07
;  PRIOR APPLICATION NUMBER: US 60/187,510
;  PRIOR FILING DATE: 2000-03-07
;  PRIOR APPLICATION NUMBER: US 60/206,129
;  PRIOR FILING DATE: 2000-05-22
;  NUMBER OF SEQ ID NOS: 1802
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1005
;   LENGTH: 31
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-801-274-1005

  Query Match             63.2%;  Score 12;  DB 10;  Length 31;
  Best Local Similarity   85.7%;  Pred. No. 3.6e+03;
```

```
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 GGTCTGCAGCGGGA 15
           |||| |||||||:|
Db      28 GGTCAGCAGCGGRA 15


RESULT 13
US-09-801-274-1006/c
; Sequence 1006, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
;  APPLICANT: Cargill, Michele
;  APPLICANT:  Ireland, James S.
;  APPLICANT:  Lander, Eric S.
;  TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
;  FILE REFERENCE: 2825.2009-001
;  CURRENT APPLICATION NUMBER: US/09/801,274
;  CURRENT FILING DATE:  2001-03-07
;  PRIOR APPLICATION NUMBER: US 60/187,510
;  PRIOR FILING DATE: 2000-03-07
;  PRIOR APPLICATION NUMBER: US 60/206,129
;  PRIOR FILING DATE: 2000-05-22
;  NUMBER OF SEQ ID NOS: 1802
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1006
;   LENGTH: 31
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-801-274-1006

  Query Match             63.2%;  Score 12;  DB 10;  Length 31;
  Best Local Similarity   85.7%;  Pred. No. 3.6e+03;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 GGTCTGCAGCGGGA 15
           |||| :|||||||
Db      21 GGTCARCAGCGGGA 8


RESULT 14
US-08-591-486B-100
; Sequence 100, Application US/08591486B
; Patent No. US20020037866A1
;  GENERAL INFORMATION:
;    APPLICANT:  Schlingensiepen, Georg F
;    APPLICANT:  Schlingensiepen, Reimar
;    APPLICANT:  Schlingensiepen, Karl-Hermann
;    APPLICANT:  Gotingen, Wolfgang Brysch
;    TITLE OF INVENTION:  A Pharmaceutical Composition
;    TITLE OF INVENTION:  Comprising Antisense-Nucleic Acid for Prevention and/or Treatm
;    TITLE OF INVENTION:  of Neuronal Injury, Degeneration and Cell Death and for the
;    TITLE OF INVENTION:  Treatment of Neoplasms
;    NUMBER OF SEQUENCES:  185
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jacobson, Price, Holman & Stern
;      STREET:  400 Seventh Street, N.W.
;      CITY:  Washington, D.C
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/591,486B
;      FILING DATE:  11-JAN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 93111059.7
;      FILING DATE:  10-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP94/02218
;      FILING DATE:  6-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Player, William E.
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  10496/P60122
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 638-6666
;      TELEFAX:  (202) 393-9350
;      TELEX:  RCA 248593 IDEA UR
;  INFORMATION FOR SEQ ID NO:  100:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  YES
US-08-591-486B-100

  Query Match             62.1%;  Score 11.8;  DB 8;  Length 20;
  Best Local Similarity   86.7%;  Pred. No. 4.4e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5 CTGCAGCGGGATGGT 19
           |||||||||||  | |
Db       2 CTGCAGCGGGAGGAT 16


RESULT 15
US-09-752-639-110
; Sequence 110, Application US/09752639
; Patent No. US20020091243A1
;  GENERAL INFORMATION:
;    APPLICANT:  Gatanaga, T.
;    APPLICANT:  Granger, G.A.
;    TITLE OF INVENTION:  Factors Altering Tumor Necrosis
;    TITLE OF INVENTION:  Factor Receptor Releasing Enzyme Activity, and Methods
;    TITLE OF INVENTION:  of Use Thereof
;    NUMBER OF SEQUENCES:  154
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/752,639
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US99/10793
;      FILING DATE:
;      APPLICATION NUMBER:  09/081,385
;      FILING DATE:
;      APPLICATION NUMBER:  08/964,747
;      FILING DATE:  05-NOV-1997
;      APPLICATION NUMBER:  60/030,761
;      FILING DATE:  06-NOV-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wu, Frank
;      REGISTRATION NUMBER:  41,386
;      REFERENCE/DOCKET NUMBER:  22000-20577.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-813-5600
;      TELEFAX:  650-494-0792
;      TELEX:  706141
```

; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-752-639-110

Query Match 62.1%; Score 11.8; DB 10; Length 20;
Best Local Similarity 86.7%; Pred. No. 4.4e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       4 TCTGCAGCGGGATGG 18
           ||||||  || |||||
Db       4 TCTGCAACGTGATGG 18
```

Search completed: November 28, 2002, 19:35:04
Job time : 39.9655 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 17:12:29 ; Search time 38.3276 Seconds
(without alignments)
152.028 Million cell updates/sec

Title: US-09-719-737-9
Perfect score: 19
Sequence: 1 gggtctgcagcgggatggt 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	12.6	66.3	32	4	US-09-194-285-5	Sequence 5, Appli
c	2	12.6	66.3	35	4	US-08-848-760B-6	Sequence 6, Appli
c	3	12.6	66.3	38	1	US-08-478-039-37	Sequence 37, Appl
c	4	12.6	66.3	38	1	US-08-476-349A-37	Sequence 37, Appl
c	5	12.6	66.3	38	3	US-08-803-085-8	Sequence 8, Appli
c	6	12.6	66.3	38	3	US-08-523-894-30	Sequence 30, Appl
c	7	12.6	66.3	41	2	US-08-761-277A-66	Sequence 66, Appl
c	8	12.6	66.3	43	4	US-08-960-190A-2	Sequence 2, Appli
c	9	12.6	66.3	43	4	US-09-042-353-399	Sequence 399, App
c	10	12.6	66.3	43	4	US-08-758-417A-249	Sequence 249, App
c	11	12.6	66.3	44	2	US-08-596-387B-40	Sequence 40, Appl
c	12	12.6	66.3	44	4	US-09-067-615-40	Sequence 40, Appl
c	13	12.6	66.3	44	5	PCT-US95-09816A-40	Sequence 40, Appl
	14	12.4	65.3	20	2	US-08-332-766A-78	Sequence 78, Appl
	15	12.4	65.3	20	3	US-09-418-640-56	Sequence 56, Appl
	16	12.4	65.3	28	1	US-07-959-946-19	Sequence 19, Appl
	17	12.4	65.3	28	1	US-08-333-577-19	Sequence 19, Appl
	18	12.4	65.3	28	5	PCT-US92-08634-19	Sequence 19, Appl
	19	12.4	65.3	47	4	US-09-641-638-1073	Sequence 1073, Ap
	20	12.2	64.2	27	6	5256545-27	Patent No. 5256545
c	21	12.2	64.2	34	1	US-08-318-193-54	Sequence 54, Appl
	22	12.2	64.2	34	1	US-08-707-793A-12	Sequence 12, Appl
	23	12.2	64.2	34	1	US-08-707-792A-12	Sequence 12, Appl
c	24	12	63.2	42	1	US-08-318-193-20	Sequence 20, Appl
c	25	12	63.2	42	6	5200327-9	Patent No. 5200327
	26	12	63.2	45	2	US-08-406-855A-17	Sequence 17, Appl
	27	12	63.2	45	3	US-09-206-899-17	Sequence 17, Appl
	28	12	63.2	45	4	US-09-688-415-22	Sequence 22, Appl
c	29	12	63.2	46	2	US-08-406-855A-18	Sequence 18, Appl
c	30	12	63.2	46	3	US-09-206-899-18	Sequence 18, Appl
c	31	12	63.2	46	4	US-09-688-415-23	Sequence 23, Appl
	32	12	63.2	50	1	US-08-318-193-21	Sequence 21, Appl
c	33	11.8	62.1	18	2	US-09-161-015-32	Sequence 32, Appl
c	34	11.8	62.1	18	4	US-09-387-341-175	Sequence 175, App
c	35	11.8	62.1	26	4	US-09-086-483A-10	Sequence 10, Appl
	36	11.8	62.1	29	4	US-08-822-999-8	Sequence 8, Appli
	37	11.8	62.1	29	4	US-09-056-285A-11	Sequence 11, Appl
c	38	11.8	62.1	30	4	US-09-025-769B-342	Sequence 342, App
	39	11.6	61.1	18	2	US-09-256-496-85	Sequence 85, Appl
c	40	11.6	61.1	25	2	US-08-859-998-1017	Sequence 1017, Ap
c	41	11.6	61.1	25	4	US-09-225-928-1017	Sequence 1017, Ap
c	42	11.6	61.1	32	1	US-08-471-033-37	Sequence 37, Appl
c	43	11.6	61.1	32	2	US-08-471-044-37	Sequence 37, Appl
c	44	11.6	61.1	32	2	US-08-463-483A-37	Sequence 37, Appl
c	45	11.6	61.1	32	2	US-08-471-046A-37	Sequence 37, Appl

ALIGNMENTS

```
RESULT 1
US-09-194-285-5/c
; Sequence 5, Application US/09194285
; Patent No. 6355479
; GENERAL INFORMATION:
;  APPLICANT: Webb, Susan R.
;  APPLICANT:  Winqvist, Ola
;  APPLICANT:  Karlsson, Lars
;  APPLICANT:  Jackson, Michael R.
;  APPLICANT:  Peterson, Per A.
;  TITLE OF INVENTION: MHC Class II Antigen Presenting Systems
;  TITLE OF INVENTION:  and Methods for Activating CD4+ T Cells
;  FILE REFERENCE: TSRI 536.1
;  CURRENT APPLICATION NUMBER: US/09/194,285
;  CURRENT FILING DATE:  1999-04-12
;  PRIOR APPLICATION NUMBER: PCT/US97/08697
;  PRIOR FILING DATE: 1997-05-22
;  PRIOR APPLICATION NUMBER: US 60/018,175
;  PRIOR FILING DATE: 1996-05-23
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 32
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthesized
US-09-194-285-5

  Query Match             66.3%;  Score 12.6;  DB 4;  Length 32;
  Best Local Similarity   78.9%;  Pred. No. 1.4e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           || ||||||| |  |||||
Db      29 GGATCTGCAGAGCCATGGT 11


RESULT 2
US-08-848-760B-6/c
; Sequence 6, Application US/08848760B
; Patent No. 6248721
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
;        NUMBER OF SEQUENCES: 33
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
;             STREET: 2421 N.W. 41st Street, Suite A-1
;             CITY: Gainesville
```

```
;            STATE: Florida
;            COUNTRY: United States of America
;            ZIP: 32606
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/848,760B
;            FILING DATE: 25-Jan-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/838,702
;            FILING DATE: 09-APR-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: PACE, DORAN R.
;            REGISTRATION NUMBER: 38,261
;            REFERENCE/DOCKET NUMBER: CNG-100C1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (352) 375-8100
;            TELEFAX: (352) 372-5800
;   INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 35 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;            DESCRIPTION: /desc = "DNA"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-848-760B-6

  Query Match             66.3%;  Score 12.6;  DB 4;  Length 35;
  Best Local Similarity   78.9%;  Pred. No. 1.4e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           || ||||||||   |||||
Db      33 GGCTCTGCAGCCACATGGT 15


RESULT 3
US-08-478-039-37/c
; Sequence 37, Application US/08478039
; Patent No. 5681722
;  GENERAL INFORMATION:
;    APPLICANT:  Newman, Roland A.
;    APPLICANT:  Hanna, Nabil
;    APPLICANT:  Raab, Ronald W.
;    TITLE OF INVENTION:  Recombinant Antibodies for Human Therapy
;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  699 Prince St.
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,039
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/379,072
;      FILING DATE:  25-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/912,292
;      FILING DATE:  10-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/856,281
;      FILING DATE:  23-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/735,064
;      FILING DATE:  25-JUL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin Esq., Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-160
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6620
;      TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  38 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens or Monkey
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  kappa light chain primer with BglII site
US-08-478-039-37

  Query Match             66.3%;  Score 12.6;  DB 1;  Length 38;
  Best Local Similarity   78.9%;  Pred. No. 1.4e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           |||||||||  |   |||||
Db      33 GGGTCTGCAACACCATGGT 15


RESULT 4
US-08-476-349A-37/c
; Sequence 37, Application US/08476349A
; Patent No. 5750105
;  GENERAL INFORMATION:
;    APPLICANT:  Newman, Roland A.
;    APPLICANT:  Hanna, Nabil
;    APPLICANT:  Raab, Ronald W.
;    TITLE OF INVENTION:  Recombinant Antibodies for Human Therapy
;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  699 Prince St.
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/476,349A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/379,072
;      FILING DATE:  25-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/912,292
;      FILING DATE:  10-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/856,281
;      FILING DATE:  23-MAR-1992
;    PRIOR APPLICATION DATA:
```

```
;       APPLICATION NUMBER:  US 07/735,064
;       FILING DATE:  25-JUL-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Teskin Esq., Robin L.
;       REGISTRATION NUMBER:  35,030
;       REFERENCE/DOCKET NUMBER:  012712-161
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  703-836-6620
;       TELEFAX:  703-836-2021
;   INFORMATION FOR SEQ ID NO:  37:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  38 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo sapiens or Monkey
;     POSITION IN GENOME:
;       CHROMOSOME/SEGMENT:  kappa light chain primer with BglII site
US-08-476-349A-37

  Query Match             66.3%;  Score 12.6;  DB 1;  Length 38;
  Best Local Similarity   78.9%;  Pred. No. 1.4e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           ||||||||| |   |||||
Db      33 GGGTCTGCAACACCATGGT 15


RESULT 5
US-08-803-085-8/c
; Sequence 8, Application US/08803085
; Patent No. 6011138
;  GENERAL INFORMATION:
;    APPLICANT:  REFF, Mitchell E.
;    APPLICANT:  KLOETZER, William S.
;    APPLICANT:  NAKAMURA, Takehiko
;    TITLE OF INVENTION:  GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
;    TITLE OF INVENTION:  ANTIBODIES AND USE THEREOF AS THERAPEUTICS
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/803,085
;      FILING DATE:  20-FEB-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-353
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  38 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-803-085-8

  Query Match             66.3%;  Score 12.6;  DB 3;  Length 38;
  Best Local Similarity   78.9%;  Pred. No. 1.4e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           ||||||||| |   |||||
Db      33 GGGTCTGCAACACCATGGT 15


RESULT 6
US-08-523-894-30/c
; Sequence 30, Application US/08523894
; Patent No. 6136310
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Nabil
;    APPLICANT:  Newman, Roland A.
;    APPLICANT:  Reff, Mitchell E.
;    TITLE OF INVENTION:  Recombinant Anti-CD4 Antibodies for Human
;    TITLE OF INVENTION:  Therapy
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22314-3187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/523,894
;      FILING DATE:  06-SEP-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-165
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6620
;      TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  38 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Human or Monkey
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  kappa light chain primer with Bgl II site
US-08-523-894-30

  Query Match             66.3%;  Score 12.6;  DB 3;  Length 38;
  Best Local Similarity   78.9%;  Pred. No. 1.4e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           ||||||||| |   |||||
Db      33 GGGTCTGCAACACCATGGT 15


RESULT 7
US-08-761-277A-66/c
; Sequence 66, Application US/08761277A
; Patent No. 5972334
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  Denney Jr., Dan W.
;    TITLE OF INVENTION:  Vaccines For Treatment Of Lymphoma And
;    TITLE OF INVENTION:  Leukemia
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/761,277A
;      FILING DATE:  06-DEC-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/644,664
;      FILING DATE:  01-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacKnight, Kamrin T.
;      REGISTRATION NUMBER:  38,230
;      REFERENCE/DOCKET NUMBER:  GENITOPE-02406
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  66:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  41 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-761-277A-66

  Query Match             66.3%;  Score 12.6;  DB 2;  Length 41;
  Best Local Similarity   78.9%;  Pred. No. 1.4e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           ||||||||| |   |||||
Db      37 GGGTCTGCAACACCATGGT 19


RESULT 8
US-08-960-190A-2/c
; Sequence 2, Application US/08960190A
; Patent No. 6232445
;  GENERAL INFORMATION:
;    APPLICANT:  Rhode, Peter R.
;    APPLICANT:  Acevedo, Jorge
;    APPLICANT:  Burkhardt, Martin
;    APPLICANT:  Jiao, Jin-an
;    APPLICANT:  Wong, Hing C.
;    TITLE OF INVENTION:  SOLUBLE MHC COMPLEXES AND
;    TITLE OF INVENTION:  METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dike, Bronstein, Roberts & Cushman, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  usa
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/960,190A
;      FILING DATE:  29-OCT-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Corless, Peter F
;      REGISTRATION NUMBER:  33,860
;      REFERENCE/DOCKET NUMBER:  48002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  43 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-960-190A-2

  Query Match             66.3%;  Score 12.6;  DB 4;  Length 43;
  Best Local Similarity   78.9%;  Pred. No. 1.4e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           || ||||||| |  |||||
Db      38 GGATCTGCAGAGCCATGGT 20


RESULT 9
US-09-042-353-399/c
; Sequence 399, Application US/09042353
; Patent No. 6255458
;  GENERAL INFORMATION:
;    APPLICANT:  Lonberg, Nils
;    APPLICANT:  Kay, Robert M.
;    TITLE OF INVENTION:  Transgenic No. 6255458-Human Animals for
;    TITLE OF INVENTION:  Producing Heterologous Antibodies
;    NUMBER OF SEQUENCES:  421
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/042,353
;      FILING DATE:  13-MAR-1998
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/810,279
;      FILING DATE:  17-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,408
;      FILING DATE:  18-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/904,068
;      FILING DATE:  23-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/990,860
;      FILING DATE:  16-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/053,131
;      FILING DATE:  26-APR-1993
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/096,762
;      FILING DATE:  22-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/155,301
;      FILING DATE:  18-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,739
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/165,699
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/209,741
;      FILING DATE:  09-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/352,322
;      FILING DATE:  07-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/544,404
;      FILING DATE:  10-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/728,463
;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US96/16433
;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/758,417
;      FILING DATE:  02-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/21803
;      FILING DATE:  01-DEC-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple, Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  014643-009040US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  399:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  43 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-09-042-353-399

  Query Match             66.3%;  Score 12.6;  DB 4;  Length 43;
  Best Local Similarity   78.9%;  Pred. No. 1.4e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           ||||||| || ||  ||||
Db      22 GGGTCTGGAGTGGATTGGT 4


RESULT 10
US-08-758-417A-249/c
; Sequence 249, Application US/08758417A
; Patent No. 6300129
;  GENERAL INFORMATION:
;       APPLICANT: Lonberg, Nils
;                  Kay, Robert M.
;       TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
;                           Producing Heterologous Antibodies
;       NUMBER OF SEQUENCES: 417
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/758,417A
;            FILING DATE: 02-Dec-1996
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/728,463
;            FILING DATE: 10-OCT-1996
;            APPLICATION NUMBER: US 08/544,404
;            FILING DATE: 10-OCT-1995
;            APPLICATION NUMBER: US 08/352,322
;            FILING DATE: 07-DEC-1994
;            APPLICATION NUMBER: US 08/209,741
;            FILING DATE: 09-MAR-1994
;            APPLICATION NUMBER: US 08/165,699
;            FILING DATE: 10-DEC-1993
;            APPLICATION NUMBER: US 08/161,739
;            FILING DATE: 03-DEC-1993
;            APPLICATION NUMBER: US 08/155,301
;            FILING DATE: 18-NOV-1993
;            APPLICATION NUMBER: US 08/096,762
;            FILING DATE: 22-JUL-1993
;            APPLICATION NUMBER: US 08/053,131
;            FILING DATE: 26-APR-1993
;            APPLICATION NUMBER: US 07/990,860
;            FILING DATE: 16-DEC-1992
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Serafini, Andrew T.
;            REGISTRATION NUMBER: 41,303
;            REFERENCE/DOCKET NUMBER: 014643-009030US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;  INFORMATION FOR SEQ ID NO: 249:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 43 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 249:
US-08-758-417A-249

  Query Match             66.3%;  Score 12.6;  DB 4;  Length 43;
  Best Local Similarity   78.9%;  Pred. No. 1.4e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           ||||||| || ||  ||||
Db      22 GGGTCTGGAGTGGATTGGT 4


RESULT 11
US-08-596-387B-40/c
; Sequence 40, Application US/08596387B
; Patent No. 5869270
;  GENERAL INFORMATION:
;    APPLICANT:  Rhode, Peter R.
;    APPLICANT:  Jiao, Jin-An
;    APPLICANT:  Burkhardt, Martin
;    APPLICANT:  Wong, Hing
;    TITLE OF INVENTION:  MHC COMPLEXES AND USES THEREOF
;    NUMBER OF SEQUENCES:  124
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dade International, Inc.
;      STREET:  1717 Deerfield Road
;      CITY:  Deerfield
```

```
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60015
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/596,387B
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/09816
;       FILING DATE:  31-JUL-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/382,454
;       FILING DATE:  01-FEB-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/283,302
;       FILING DATE:  29-JUL-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Pearson, Louise S.
;       REGISTRATION NUMBER:  32,369
;       REFERENCE/DOCKET NUMBER:  STR-4665-CIP2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (708) 267-5300
;       TELEFAX:  (708) 267-5376
;   INFORMATION FOR SEQ ID NO:  40:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  44 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  unknown
;       TOPOLOGY:  unknown
US-08-596-387B-40

  Query Match             66.3%;  Score 12.6;  DB 2;  Length 44;
  Best Local Similarity   78.9%;  Pred. No. 1.4e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           || ||||||| |  |||||
Db      39 GGATCTGCAGAGCCATGGT 21


RESULT 12
US-09-067-615-40/c
; Sequence 40, Application US/09067615
; Patent No. 6309645
;  GENERAL INFORMATION:
;     APPLICANT:  Rhode, Peter R.
;     APPLICANT:  Jiao, Jin-An
;     APPLICANT:  Burkhardt, Martin
;     APPLICANT:  Wong, Hing
;     TITLE OF INVENTION:  MHC COMPLEXES AND USES THEREOF
;     NUMBER OF SEQUENCES:  124
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Dade International, Inc.
;       STREET:  1717 Deerfield Road
;       CITY:  Deerfield
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60015
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/067,615
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/596,387
;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/382,454
;       FILING DATE:  01-FEB-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/283,302
;       FILING DATE:  29-JUL-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Pearson, Louise S.
;       REGISTRATION NUMBER:  32,369
;       REFERENCE/DOCKET NUMBER:  STR-4665-CIP2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (708) 267-5300
;       TELEFAX:  (708) 267-5376
;   INFORMATION FOR SEQ ID NO:  40:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  44 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  unknown
;       TOPOLOGY:  unknown
US-09-067-615-40

  Query Match             66.3%;  Score 12.6;  DB 4;  Length 44;
  Best Local Similarity   78.9%;  Pred. No. 1.4e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           || ||||||| |  |||||
Db      39 GGATCTGCAGAGCCATGGT 21


RESULT 13
PCT-US95-09816A-40/c
; Sequence 40, Application PC/TUS9509816A
;  GENERAL INFORMATION:
;     APPLICANT:  Wong, Hing C.
;     APPLICANT:  Rhode, Peter R.
;     APPLICANT:  Widanz, Jon A.
;     APPLICANT:  Grammer, Susan
;     APPLICANT:  Edwards, Ana C.
;     APPLICANT:  Chavaillaz, Pierre-Andre
;     APPLICANT:  Jiao, Jin-An
;     TITLE OF INVENTION:  MHC COMPLEXES AND USES THEREOF
;     NUMBER OF SEQUENCES:  123
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Dade International, Inc.
;       STREET:  1717 Deerfield Road
;       CITY:  Deerfield
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60015
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/09816A
;       FILING DATE:  31-JUL-1995
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/382,454
;       FILING DATE:  01-FEB-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/283,302
;       FILING DATE:  29-JUL-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Pearson, Louise S.
;       REGISTRATION NUMBER:  32,369
;       REFERENCE/DOCKET NUMBER:  STR-4665-CIP2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (708) 267-5300
```

```
;      TELEFAX:  (708) 267-5376
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  44 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
PCT-US95-09816A-40

  Query Match             66.3%;  Score 12.6;  DB 5;  Length 44;
  Best Local Similarity   78.9%;  Pred. No. 1.4e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           || ||||||| |  |||||
Db      39 GGATCTGCAGAGCCATGGT 21


RESULT 14
US-08-332-766A-78
; Sequence 78, Application US/08332766A
; Patent No. 5843647
;  GENERAL INFORMATION:
;    APPLICANT:  JEFFREYS, Alec J.
;    APPLICANT:  ARMOUR, John
;    TITLE OF INVENTION:  SIMPLE TANDEM REPEATS
;    NUMBER OF SEQUENCES:  125
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CUSHMAN DARBY & CUSHMAN, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D. C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/332,766A
;      FILING DATE:  01-NOV-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9326052.9
;      FILING DATE:  21-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BIRD, Donald J.
;      REGISTRATION NUMBER:  25,323
;      REFERENCE/DOCKET NUMBER:  217211/M94/0434/GB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 861-3000
;      TELEFAX:  (202) 822-0944
;      TELEX:  6714627 CUSH
;  INFORMATION FOR SEQ ID NO:  78:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-332-766A-78

  Query Match             65.3%;  Score 12.4;  DB 2;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 1.7e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 GTCTGCAGCGGGAT 16
           | ||||||||||||
Db       2 GACTGCAGCGGGAT 15


RESULT 15
US-09-418-640-56
; Sequence 56, Application US/09418640
; Patent No. 6140125
; GENERAL INFORMATION:
;  APPLICANT: Jennifer K. Taylor
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF BCL-6 EXPRESSION
;  FILE REFERENCE: RTS-0102
;  CURRENT APPLICATION NUMBER: US/09/418,640
;  CURRENT FILING DATE: 1999-10-15
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 56
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-418-640-56

  Query Match             65.3%;  Score 12.4;  DB 3;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 1.7e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGG 14
           ||||||||||||| |
Db       7 GGGTCTGCAGCGTG 20


Search completed: November 28, 2002, 19:32:50
Job time : 39.3276 secs
```

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 15:32:44 ; Search time 176.241 Seconds
(without alignments)
242.780 Million cell updates/sec

Title: US-09-719-737-9
Perfect score: 19
Sequence: 1 gggtctgcagcgggatggt 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	19	100.0	19	21	AAZ56193	Oligonucleotide 10
	2	18	94.7	19	21	AAZ56194	Oligonucleotide 10
	3	18	94.7	19	21	AAZ56195	Oligonucleotide 10
	4	17	89.5	19	21	AAZ56199	Oligonucleotide 10
	5	16	84.2	19	21	AAZ56196	Oligonucleotide 11
	6	14.8	77.9	27	22	AAH45301	Human Bcl-2 mutage
	7	14.2	74.7	20	24	AAS96640	Telomerase reverse
c	8	14.2	74.7	34	21	AAA30293	R. eutropha toluen
c	9	13.4	70.5	20	24	ABA81692	PCR primer KP108.
	10	13.4	70.5	42	22	AAF81879	HBV gene hybridisa
	11	13.4	70.5	47	17	AAT34741	PCR primer OPR141
	12	13.2	69.5	27	22	AAH45300	Human Bcl-2 mutage
	13	13.2	69.5	27	24	ABK47064	Adenovirus vector
c	14	13.2	69.5	33	16	AAQ97259	ATF-2 5' bridging
	15	13.2	69.5	38	17	AAT33615	Murine VRF167 mRNA
	16	13	68.4	19	21	AAZ56197	Oligonucleotide 10
c	17	12.8	67.4	25	18	AAT85301	Human chemotactic
	18	12.8	67.4	50	22	AAH89733	Human coding sequ
	19	12.6	66.3	21	22	AAH62345	GRIK1 polymorphism
c	20	12.6	66.3	32	19	AAV12065	Murine IAd beta ch
c	21	12.6	66.3	33	22	AAF55037	PCR primer used to
c	22	12.6	66.3	33	22	AAF75850	PCR primer RG972.
c	23	12.6	66.3	33	22	AAF24095	Porcine GM-CSF RT-
c	24	12.6	66.3	35	20	AAV83185	Primer for amplify
c	25	12.6	66.3	35	21	AAA90485	Human GM-CSF PCR p
c	26	12.6	66.3	36	22	AAF56666	Human GM-CSF cDNA
c	27	12.6	66.3	37	21	AAZ55603	Feline GMCSF sense
c	28	12.6	66.3	38	14	AAQ35916	Human/monkey kappa
c	29	12.6	66.3	38	18	AAT95141	Human or monkey Ig
c	30	12.6	66.3	38	18	AAT92217	Monkey/human kappa
c	31	12.6	66.3	38	18	AAT62888	Human or monkey ka
c	32	12.6	66.3	38	19	AAV33314	Anti-CD23 5E8 anti
c	33	12.6	66.3	38	19	AAV31401	Human or monkey ka
c	34	12.6	66.3	38	19	AAV23779	Primer for Anti-CD
c	35	12.6	66.3	38	19	AAV05663	Human/monkey kappa
c	36	12.6	66.3	39	20	AAZ40438	Human RAD1 gene pr
c	37	12.6	66.3	39	21	AAC73407	Single base extens
c	38	12.6	66.3	41	18	AAT97209	Kappa chain variab
c	39	12.6	66.3	43	18	AAT78831	Gamma heavy chain
c	40	12.6	66.3	43	19	AAV39272	Primer O-543 used
c	41	12.6	66.3	43	20	AAZ22026	Oligonucleotide us
c	42	12.6	66.3	43	20	AAX89047	PCR primer OPR132
c	43	12.6	66.3	44	17	AAT34718	PCR primer OPR132
c	44	12.6	66.3	44	18	AAT86972	Primer used in MHC
c	45	12.6	66.3	44	23	AAF28959	Equine GM-CSF gene

ALIGNMENTS

RESULT 1
AAZ56193
ID AAZ56193 standard; DNA; 19 BP.
XX
AC AAZ56193;
XX
DT 28-MAR-2000 (first entry)
XX
DE Oligonucleotide 107A for IL-3/IL-5/GM-CSF receptor expression inhibition.
XX
KW Interleukin-3; IL-3; interleukin-5; IL-5; antisense oligonucleotide;
KW asthma; allergy; cancer; receptor expression inhibitor; cytokine;
KW inflammation; hypereosinophilia; eosinophil proliferation;
KW granulocyte macrophage colony stimulating factor; GM-CSF; ss.
XX
OS Homo sapiens.
XX
PN WO9966037-A2.
XX
PD 23-DEC-1999.
XX
PF 17-JUN-1999; 99WO-CA00572.
XX
PR 17-JUN-1998; 98CA-2235420.
XX
PA (REEX-) RECH EXPERTISES & DEV MEDICAUX PARENZ IN.
XX
PI Renzi P;
XX
DR WPI; 2000-097743/08.
XX
PT Antisense oligonucleotides directed to CCR3, interleukin or granulocyte

```
PT   macrophage colony stimulating factor receptors, used for treating or
PT   preventing asthma, allergies, hypereosinophilia, inflammation or cancer
PT    -
XX
PS   Claim 5; Page 23; 72pp; English.
XX
CC   This is an antisense oligonucleotide directed against the common beta
CC   subunit of the interleukin-3 (IL-3) receptor, the interleukin-5 (IL-5)
CC   receptor and the granulocyte macrophage colony stimulating factor
CC   (GM-CSF) receptor. The antisense oligonucleotide inhibits IL-3, IL-5
CC   and GM-CSF receptor expression. IL-3, IL-5 and GM-CSF are cytokines
CC   involved in eosinophil proliferation and survival, they are increased in
CC   asthma and atopic diseases, and are also involved in the indefinite
CC   proliferation of certain neoplastic diseases. The invention relates to
CC   antisense oligonucleotides directed against a nucleic acid sequence
CC   encoding either a chemokine receptor (CCR3), a common subunit of
CC   interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common
CC   subunit of IL-3, IL-5 and GM-CSF receptors. The antisense
CC   oligonucleotides can be used in the treatment or prevention of asthma,
CC   allergy, hypereosinophilia, general inflammation or cancer.
XX
SQ   Sequence 19 BP; 2 A; 3 C; 10 G; 4 T; 0 other;

  Query Match             100.0%;  Score 19;  DB 21;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 8.5;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           |||||||||||||||||||
Db       1 GGGTCTGCAGCGGGATGGT 19


RESULT 2
AAZ56194
ID   AAZ56194 standard; DNA; 19 BP.
XX
AC   AAZ56194;
XX
DT   28-MAR-2000  (first entry)
XX
DE   Oligonucleotide 106 for IL-3/IL-5/GM-CSF receptor expression inhibition.
XX
KW   Interleukin-3; IL-3; interleukin-5; IL-5; antisense oligonucleotide;
KW   asthma; allergy; cancer; receptor expression inhibitor; cytokine;
KW   inflammation; hypereosinophilia; eosinophil proliferation;
KW   granulocyte macrophage colony stimulating factor; GM-CSF; ss.
XX
OS   Homo sapiens.
XX
PN   WO9966037-A2.
XX
PD   23-DEC-1999.
XX
PF   17-JUN-1999;   99WO-CA00572.
XX
PR   17-JUN-1998;   98CA-2235420.
XX
PA   (REEX-) RECH EXPERTISES & DEV MEDICAUX PARENZ IN.
XX
PI   Renzi P;
XX
DR   WPI; 2000-097743/08.
XX
PT   Antisense oligonucleotides directed to CCR3, interleukin or granulocyte
PT   macrophage colony stimulating factor receptors, used for treating or
PT   preventing asthma, allergies, hypereosinophilia, inflammation or cancer
PT    -
XX
PS   Claim 5; Page 25; 72pp; English.
XX
CC   This is an antisense oligonucleotide directed against the common beta
CC   subunit of the interleukin-3 (IL-3) receptor, the interleukin-5 (IL-5)
CC   receptor and the granulocyte macrophage colony stimulating factor
CC   (GM-CSF) receptor. The antisense oligonucleotide inhibits IL-3, IL-5
CC   and GM-CSF receptor expression. IL-3, IL-5 and GM-CSF are cytokines
CC   involved in eosinophil proliferation and survival, they are increased in
CC   asthma and atopic diseases, and are also involved in the indefinite
CC   proliferation of certain neoplastic diseases. The invention relates to
CC   antisense oligonucleotides directed against a nucleic acid sequence
CC   encoding either a chemokine receptor (CCR3), a common subunit of
CC   interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common
CC   subunit of IL-3, IL-5 and GM-CSF receptors. The antisense
CC   oligonucleotides can be used in the treatment or prevention of asthma,
CC   allergy, hypereosinophilia, general inflammation or cancer.
XX
SQ   Sequence 19 BP; 2 A; 3 C; 9 G; 5 T; 0 other;

  Query Match             94.7%;  Score 18;  DB 21;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 GGTCTGCAGCGGGATGGT 19
           ||||||||||||||||||
Db       1 GGTCTGCAGCGGGATGGT 18


RESULT 3
AAZ56195
ID   AAZ56195 standard; DNA; 19 BP.
XX
AC   AAZ56195;
XX
DT   28-MAR-2000  (first entry)
XX
DE   Oligonucleotide 108 for IL-3/IL-5/GM-CSF receptor expression inhibition.
XX
KW   Interleukin-3; IL-3; interleukin-5; IL-5; antisense oligonucleotide;
KW   asthma; allergy; cancer; receptor expression inhibitor; cytokine;
KW   inflammation; hypereosinophilia; eosinophil proliferation;
KW   granulocyte macrophage colony stimulating factor; GM-CSF; ss.
XX
OS   Homo sapiens.
XX
PN   WO9966037-A2.
XX
PD   23-DEC-1999.
XX
PF   17-JUN-1999;   99WO-CA00572.
XX
PR   17-JUN-1998;   98CA-2235420.
XX
PA   (REEX-) RECH EXPERTISES & DEV MEDICAUX PARENZ IN.
XX
PI   Renzi P;
XX
DR   WPI; 2000-097743/08.
XX
PT   Antisense oligonucleotides directed to CCR3, interleukin or granulocyte
PT   macrophage colony stimulating factor receptors, used for treating or
PT   preventing asthma, allergies, hypereosinophilia, inflammation or cancer
PT    -
XX
PS   Claim 5; Page 25; 72pp; English.
XX
CC   This is an antisense oligonucleotide directed against the common beta
CC   subunit of the interleukin-3 (IL-3) receptor, the interleukin-5 (IL-5)
CC   receptor and the granulocyte macrophage colony stimulating factor
CC   (GM-CSF) receptor. The antisense oligonucleotide inhibits IL-3, IL-5
CC   and GM-CSF receptor expression. IL-3, IL-5 and GM-CSF are cytokines
CC   involved in eosinophil proliferation and survival, they are increased in
CC   asthma and atopic diseases, and are also involved in the indefinite
CC   proliferation of certain neoplastic diseases. The invention relates to
CC   antisense oligonucleotides directed against a nucleic acid sequence
CC   encoding either a chemokine receptor (CCR3), a common subunit of
CC   interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common
CC   subunit of IL-3, IL-5 and GM-CSF receptors. The antisense
```

CC oligonucleotides can be used in the treatment or prevention of asthma,
CC allergy, hypereosinophilia, general inflammation or cancer.
XX
SQ Sequence 19 BP; 3 A; 3 C; 10 G; 3 T; 0 other;

Query Match 94.7%; Score 18; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTCTGCAGCGGGATGG 18
||||||||||||||||||
Db 2 GGGTCTGCAGCGGGATGG 19

RESULT 4
AAZ56199
ID AAZ56199 standard; DNA; 19 BP.
XX
AC AAZ56199;
XX
DT 28-MAR-2000 (first entry)
XX
DE Oligonucleotide 105 for IL-3/IL-5/GM-CSF receptor expression inhibition.
XX
KW Interleukin-3; IL-3; interleukin-5; IL-5; antisense oligonucleotide;
KW asthma; allergy; cancer; receptor expression inhibitor; cytokine;
KW inflammation; hypereosinophilia; eosinophil proliferation;
KW granulocyte macrophage colony stimulating factor; GM-CSF; ss.
XX
OS Homo sapiens.
XX
PN WO9966037-A2.
XX
PD 23-DEC-1999.
XX
PF 17-JUN-1999; 99WO-CA00572.
XX
PR 17-JUN-1998; 98CA-2235420.
XX
PA (REEX-) RECH EXPERTISES & DEV MEDICAUX PARENZ IN.
XX
PI Renzi P;
XX
DR WPI; 2000-097743/08.
XX
PT Antisense oligonucleotides directed to CCR3, interleukin or granulocyte
PT macrophage colony stimulating factor receptors, used for treating or
PT preventing asthma, allergies, hypereosinophilia, inflammation or cancer
PT -
XX
PS Claim 5; Page 25; 72pp; English.
XX
CC This is an antisense oligonucleotide directed against the common beta
CC subunit of the interleukin-3 (IL-3) receptor, the interleukin-5 (IL-5)
CC receptor and the granulocyte macrophage colony stimulating factor
CC (GM-CSF) receptor. The antisense oligonucleotide inhibits IL-3, IL-5
CC and GM-CSF receptor expression. IL-3, IL-5 and GM-CSF are cytokines
CC involved in eosinophil proliferation and survival, they are increased in
CC asthma and atopic diseases, and are also involved in the indefinite
CC proliferation of certain neoplastic diseases. The invention relates to
CC antisense oligonucleotides directed against a nucleic acid sequence
CC encoding either a chemokine receptor (CCR3), a common subunit of
CC interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common
CC subunit of IL-3, IL-5 and GM-CSF receptors. The antisense
CC oligonucleotides can be used in the treatment or prevention of asthma,
CC allergy, hypereosinophilia, general inflammation or cancer.
XX
SQ Sequence 19 BP; 2 A; 3 C; 8 G; 6 T; 0 other;

Query Match 89.5%; Score 17; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GTCTGCAGCGGGATGGT 19
|||||||||||||||||
Db 1 GTCTGCAGCGGGATGGT 17

RESULT 5
AAZ56196
ID AAZ56196 standard; DNA; 19 BP.
XX
AC AAZ56196;
XX
DT 28-MAR-2000 (first entry)
XX
DE Oligonucleotide 110 for IL-3/IL-5/GM-CSF receptor expression inhibition.
XX
KW Interleukin-3; IL-3; interleukin-5; IL-5; antisense oligonucleotide;
KW asthma; allergy; cancer; receptor expression inhibitor; cytokine;
KW inflammation; hypereosinophilia; eosinophil proliferation;
KW granulocyte macrophage colony stimulating factor; GM-CSF; ss.
XX
OS Homo sapiens.
XX
PN WO9966037-A2.
XX
PD 23-DEC-1999.
XX
PF 17-JUN-1999; 99WO-CA00572.
XX
PR 17-JUN-1998; 98CA-2235420.
XX
PA (REEX-) RECH EXPERTISES & DEV MEDICAUX PARENZ IN.
XX
PI Renzi P;
XX
DR WPI; 2000-097743/08.
XX
PT Antisense oligonucleotides directed to CCR3, interleukin or granulocyte
PT macrophage colony stimulating factor receptors, used for treating or
PT preventing asthma, allergies, hypereosinophilia, inflammation or cancer
PT -
XX
PS Claim 5; Page 25; 72pp; English.
XX
CC This is an antisense oligonucleotide directed against the common beta
CC subunit of the interleukin-3 (IL-3) receptor, the interleukin-5 (IL-5)
CC receptor and the granulocyte macrophage colony stimulating factor
CC (GM-CSF) receptor. The antisense oligonucleotide inhibits IL-3, IL-5
CC and GM-CSF receptor expression. IL-3, IL-5 and GM-CSF are cytokines
CC involved in eosinophil proliferation and survival, they are increased in
CC asthma and atopic diseases, and are also involved in the indefinite
CC proliferation of certain neoplastic diseases. The invention relates to
CC antisense oligonucleotides directed against a nucleic acid sequence
CC encoding either a chemokine receptor (CCR3), a common subunit of
CC interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common
CC subunit of IL-3, IL-5 and GM-CSF receptors. The antisense
CC oligonucleotides can be used in the treatment or prevention of asthma,
CC allergy, hypereosinophilia, general inflammation or cancer.
XX
SQ Sequence 19 BP; 3 A; 4 C; 9 G; 3 T; 0 other;

Query Match 84.2%; Score 16; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTCTGCAGCGGGAT 16
||||||||||||||||
Db 4 GGGTCTGCAGCGGGAT 19

RESULT 6
AAH45301
ID AAH45301 standard; DNA; 27 BP.
XX

```
AC   AAH45301;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human Bcl-2 mutagenic primer oligo-4 for S70D substitution.
XX
KW   Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; primer; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200142459-A1.
XX
PD   14-JUN-2001.
XX
PF   07-DEC-2000; 2000WO-JP08667.
XX
PR   09-DEC-1999;   99JP-0350427.
XX
PA   (HISM ) HISAMITSU PHARM CO LTD.
XX
PI   Shibazaki F,  Kuma H;
XX
DR   WPI; 2001-381681/40.
XX
PT   New apoptosis inhibitors, useful for treating apoptosis related
PT   disorders -
XX
PS   Example 1; Page 10; 43pp; Japanese.
XX
CC   The invention relates to an apoptosis inhibitor comprising the
CC   amino acid sequence of Bcl-2 protein in which at least one serine
CC   residue is substituted by alanine or aspartic acid. The protein has
CC   increased apoptosis inhibitory activity compared with the wild type
CC   Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment
CC   of disorders caused by apoptosis. The present sequence was used to
CC   create a mutant Bcl-2 protein of the invention.
XX
SQ   Sequence 27 BP; 2 A; 8 C; 12 G; 5 T; 0 other;

  Query Match             77.9%;  Score 14.8;  DB 22;  Length 27;
  Best Local Similarity   88.9%;  Pred. No. 8.7e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GGTCTGCAGCGGGATGGT 19
           |||||||||||||  |||
Db       1 GGTCTGCAGCGGGTCGGT 18


RESULT 7
AAS96640
ID   AAS96640 standard; DNA; 20 BP.
XX
AC   AAS96640;
XX
DT   09-APR-2002  (first entry)
XX
DE   Telomerase reverse transcriptase, antisense oligonucleotide #50.
XX
KW   Telomerase reverse transcriptase; TERT; cytostatic; apoptosis;
KW   cell growth inhibitor; antisense oligonucleotide;
KW   antisense technology; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200188198-A1.
XX
PD   22-NOV-2001.
XX
PF   15-MAY-2001; 2001WO-US15774.
XX
PR   16-MAY-2000; 2000US-0572423.
PR   07-DEC-2000; 2000US-0733294.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Gaarde WA,  Freier SM,  Wancewicz E;
XX
DR   WPI; 2002-075321/10.
XX
PT   New compound targeted to nucleic acid molecule encoding telomerase
PT   transcriptase (TERT), which specifically hybridises with and inhibits
PT   expression of TERT, useful for modulating apoptosis and inhibiting cell
PT   growth -
XX
PS   Example 19; Page 91; 154pp; English.
XX
CC   The invention describes a compound, 8-50 nucleobases in length targeted
CC   to a nucleic acid molecule encoding human TERT (telomerase reverse
CC   transcriptase), where the compound specifically hybridises with and
CC   inhibits the expression of TERT. A series of oligonucleotides were
CC   designed to target different regions of the human TERT RNA. These were
CC   20 nucleotides in length and composed of a central gap region consisting
CC   of ten 2'-deoxynucleotides, flanked on both sides (5' and 3' directions)
CC   by five-nucleotide wings. The wings were composed of 2'-methoxyethyl
CC   (2'-MOE) nucleotides. The compounds were analysed for their effect on
CC   human TERT mRNA levels by reverse transcriptase (RT)-polymerase chain
CC   reaction (PCR). The compound is useful for inhibiting the expression of
CC   TERT in cells or tissues, for treating a human having disease or
CC   condition associated with TERT, for modulating apoptosis, for inhibiting
CC   cell growth (preferably, cancer cell growth), in antisense therapy and
CC   for diagnostics and therapeutics. This sequence is an antisense
CC   oligonucleotide used to modulate the activity of nucleic acid molecules
CC   encoding TERT, described in the method of the invention.
XX
SQ   Sequence 20 BP; 2 A; 5 C; 8 G; 5 T; 0 other;

  Query Match             74.7%;  Score 14.2;  DB 24;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           |||||| || | |||||||
Db       1 GGGTCTCCACCTGGATGGT 19


RESULT 8
AAA30293/c
ID   AAA30293 standard; DNA; 34 BP.
XX
AC   AAA30293;
XX
DT   11-SEP-2000  (first entry)
XX
DE   R. eutropha toluene monooxygenase tomK primer, tom-K.
XX
KW   Toluene monooxygenase; carcinogen; halogenated aliphatic hydrocarbon;
KW   halogenated aromatic hydrocarbon; environmental pollution;
KW   environmental remediation; enzyme; tomK primer;
KW   site-directed mutagenesis; ss.
XX
OS   Ralstonia eutropha strain TB64.
XX
PN   EP1006191-A2.
XX
PD   07-JUN-2000.
XX
PF   03-DEC-1999;   99EP-0124209.
XX
PR   03-DEC-1998;   98JP-0344506.
XX
PA   (CANO ) CANON KK.
XX
PI   Yano T,  Nomoto T,  Imamura T;
XX
```

DR WPI; 2000-378265/33.
XX
PT New polynucleotide encoding toluene monooxygenase for generating
PT transformants useful for decontaminating environments polluted with
PT e.g. aromatic hydrocarbons -
XX
PS Example 6; Page 20; 54pp; English.
XX
CC Toluene monooxygenase catalyses the degradation of environmental
CC pollutants such as halogenated aliphatic compounds e.g.
CC tetrachloroethylene (PCE), trichloroethylene (TCE) and dichloroethylene
CC (DCE) and/or aromatic hydrocarbons e.g. toluene, benzene, phenol,
CC cresol. These pollutants are considered to be potential carcinogens. A
CC DNA fragment of about 5.3 Kb containing a toluene monooxygenase (Tom)
CC gene from Ralstonia eutropha strain TB64 has been isolated (AAA30292).
CC The sequence in AAA30292 contains seven coding sequences, one of which
CC is tomK. TomK protein is an enhancer of toluene monooxygenase activity.
CC The present sequence is the tom-K primer. This primer was used to
CC introduce a NcoI restriction site into the tomK coding sequence by PCR.
CC After the introduction of the restriction sites, the coding sequence
CC could be cloned into expression vectors pSE280 and pSE380. These
CC recombinant vectors were then used in the transformation of microbial
CC cells conferring them with toluene monooxygenase activity. These
CC recombinant cells would therefore be useful in environmental
CC remediation.
XX
SQ Sequence 34 BP; 8 A; 14 C; 7 G; 5 T; 0 other;

Query Match 74.7%; Score 14.2; DB 21; Length 34;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGTCTGCAGCGGGATGGT 19
||||||||||.|.|||||
Db 31 GGGTCTGCAGGGCCATGGT 13

RESULT 9
ABA81692/c
ID ABA81692 standard; DNA; 20 BP.
XX
AC ABA81692;
XX
DT 25-JAN-2002 (first entry)
XX
DE PCR primer KP108.
XX
KW Aldehyde-dehydrogenase; enzyme; phenanthrene; anthracene; PCR primer;
KW aromatic dihydrodiol dehydrogenase; aromatic diol oxygenase;
KW hydratase-aldorase; ss.
XX
OS Nocardioides sp. KP7.
XX
PN JP2001245662-A.
XX
PD 11-SEP-2001.
XX
PF 03-MAR-2000; 2000JP-0059523.
XX
PR 03-MAR-2000; 2000JP-0059523.
XX
PA (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
XX
DR WPI; 2002-002935/01.
XX
PT Genes and proteins involved in the upstream of the pathway of
PT degradation of a polycyclic aromatic compound -
XX
PS Example 4; Page 6; 47pp; Japanese.
XX
CC The present invention relates to coding sequences for proteins such as
CC aromatic dihydrodiol dehydrogenase, aromatic diol oxygenase,
CC hydratase-aldorase and aldehyde-dehydrogenase (ABA01198-ABA01201 and
CC AAM52344-AAM52347), which are involved in the degradation of polycyclic
CC aromatic compounds. The enzymes are useful as reagents for converting the
CC metabolite intermediates of polycyclic aromatic compounds such as
CC phenanthrene and anthracene. The present sequence is a PCR primer, which
CC was used in an example from the present invention.
XX
SQ Sequence 20 BP; 5 A; 9 C; 5 G; 1 T; 0 other;

Query Match 70.5%; Score 13.4; DB 24; Length 20;
Best Local Similarity 93.3%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGTCTGCAGCGGGAT 16
||||||||||||| |
Db 15 GGTCTGCAGCGGGTT 1

RESULT 10
AAF81879
ID AAF81879 standard; DNA; 42 BP.
XX
AC AAF81879;
XX
DT 08-JUN-2001 (first entry)
XX
DE HBV gene hybridisation detection related probe/primer #12.
XX
KW Hepatitis B virus; HBV; gene hybridisation; detection; probe; primer;
KW amplification; ss.
XX
OS Hepatitis B virus.
XX
PN CN1274847-A.
XX
PD 29-NOV-2000.
XX
PF 02-JUN-2000; 2000CN-0116306.
XX
PR 02-JUN-2000; 2000CN-0116306.
XX
PA (CHAN-) CHANGZHENG HOSPITAL SHANGHAI.
XX
PI Miao X, Kong X, Qi Z;
XX
DR WPI; 2001-211778/22.
XX
PT Making a marker signal amplifying probe for gene hybridization
PT detection of e.g. hepatitis B, comprises a polymerase chain reaction -
XX
PS Example 2; Page 9; 18pp; Chinese.
XX
CC The present invention describes a method for the design and synthesis of
CC a marker signal amplifying probe and primer. The method comprises:
CC (a) connecting the probe and primer through a connecting arm;
CC (b) polymerase chain reaction (PCR) of probe/primer as an upstream
CC primer, one gene template and a downstream primer to obtain some DNA
CC section with one single-chain end and other double-chainpart; and
CC (c) PCR to add a marker into double chain. The amplifying probe may be
CC used in various in vitro gene hybridisation detecting technology. The
CC method of the present invention is simple and has adjustable
CC amplification, and when used in detecting hepatitis B virus (HBV)
CC genome, it has high sensitivity and strong specificity. AAF81868 to
CC AAF81893 represent oligonucleotide sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 42 BP; 12 A; 8 C; 13 G; 9 T; 0 other;

Query Match 70.5%; Score 13.4; DB 22; Length 42;
Best Local Similarity 93.3%; Pred. No. 4.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CTGCAGCGGGATGGT 19
||||||||| |||||

```
Db      18 CTGCAGCGGTATGGT 32


RESULT 11
AAT34741
ID   AAT34741 standard; DNA; 47 BP.
XX
AC   AAT34741;
XX
DT   23-SEP-1996  (first entry)
XX
DE   PCR primer OPR141 used in construction of MHC fusion complex vector.
XX
KW   MHC; major histocompatibility complex; PCR; polymerase chain reaction;
KW   T cell activity modulator; antagonist; immune disorder; allergy;
KW   multiple sclerosis; insulin-dependent diabetes mellitus;
KW   rheumatoid arthritis; myasthenia gravis; ss.
XX
OS   Synthetic.
XX
PN   WO9604314-A1.
XX
PD   15-FEB-1996.
XX
PF   31-JUL-1995;   95WO-US09816.
XX
PR   01-FEB-1995;   95US-0382454.
PR   29-JUL-1994;   94US-0283302.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Chavaillaz P-A,  Edwards AC,  Grammer S,  Jiao J-A,  Rhode PR;
PI   Weidanz JA,  Wong HC;
XX
DR   WPI; 1996-129343/13.
XX
PT   Major histocompatibility complex fusion complex for modulating T
PT   cell activity  - used in the treatment of immune disorders, e.g.
PT   multiple sclerosis, IDDM and rheumatoid arthritis
XX
PS   Example 1; Fig 8; 210pp; English.
XX
CC   AAT34735-T34750 are PCR primers used in the construction of MHC fusion
CC   complexes capable of modulating T cell activity. The MHC fusion complex
CC   comprises a MHC molecule containing a peptide-binding groove and a
CC   presenting peptide covalently linked to the MHC molecule and opt. a
CC   transmembrane domain. Multivalent MHC fusion complexes may also be
CC   made comprising 2 or more linked MHC fusion complexes. DNA encoding
CC   a MHC fusion complex may be cloned into a host cell to express the
CC   complex. The transformed cells may then be used to identify peptides
CC   that modulate, pref. antagonise, T cell activity. DNA encoding a MHC
CC   fusion complex  or a single chain fusion molecule may be used to
CC   vaccinate a mammal against a targeted disorder. The fusion
CC   complexes may be used to suppress an immune response in an animal
CC   suffering from an immune disorder e.g. multiple sclerosis, insulin-
CC   dependent diabetes mellitus, rheumatoid arthritis, myasthenia
CC   gravis or chronic allergies. The complexes may also be used in the
CC   treatment of livestock and pets such as cats and dogs. The MHC
CC   fusion complexes can be produced such that they contain a single
CC   antigenic peptide including one of known structure, additionally a
CC   wide range of peptides can be presented for T cell interaction.
XX
SQ   Sequence 47 BP; 9 A; 11 C; 18 G; 8 T; 1 other;

  Query Match             70.5%;  Score 13.4;  DB 17;  Length 47;
  Best Local Similarity   78.9%;  Pred. No. 4.1e+03;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           ||  ||||||:|||||| |
Db      18 GGCGCTGCAGBGGGATGTT 36
```

```
RESULT 12
AAH45300
ID   AAH45300 standard; DNA; 27 BP.
XX
AC   AAH45300;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human Bcl-2 mutagenic primer oligo-3 for S70A substitution.
XX
KW   Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; primer; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200142459-A1.
XX
PD   14-JUN-2001.
XX
PF   07-DEC-2000; 2000WO-JP08667.
XX
PR   09-DEC-1999;   99JP-0350427.
XX
PA   (HISM ) HISAMITSU PHARM CO LTD.
XX
PI   Shibazaki F,  Kuma H;
XX
DR   WPI; 2001-381681/40.
XX
PT   New apoptosis inhibitors, useful for treating apoptosis related
PT   disorders  -
XX
PS   Example 1; Page 10; 43pp; Japanese.
XX
CC   The invention relates to an apoptosis inhibitor comprising the
CC   amino acid sequence of Bcl-2 protein in which at least one serine
CC   residue is substituted by alanine or aspartic acid. The protein has
CC   increased apoptosis inhibitory activity compared with the wild type
CC   Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment
CC   of disorders caused by apoptosis. The present sequence was used to
CC   create a mutant Bcl-2 protein of the invention.
XX
SQ   Sequence 27 BP; 2 A; 9 C; 12 G; 4 T; 0 other;

  Query Match             69.5%;  Score 13.2;  DB 22;  Length 27;
  Best Local Similarity   83.3%;  Pred. No. 5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 GGTCTGCAGCGGGATGGT 19
           ||||||||||||   |||
Db       1 GGTCTGCAGCGGCGCGGT 18


RESULT 13
ABK47064
ID   ABK47064 standard; DNA; 27 BP.
XX
AC   ABK47064;
XX
DT   05-JUN-2002  (first entry)
XX
DE   Adenovirus vector E3 region deletion PCR primer 4.
XX
KW   Adenovirus vector library; ss; primer; high throughput screening;
KW   RCA; replication competent adenovirus; PCR.
XX
OS   Mastadenovirus Ad5.
XX
PN   US6340595-B1.
XX
PD   22-JAN-2002.
XX
PF   21-JUL-1999;   99US-0358036.
```

XX
PR 12-JUN-1998; 98US-0097239.
XX
PA (GALA-) GALAPAGOS GENOMICS NV.
XX
PI Vogels R, Bout A, Van Es H, Schouten G;
XX
DR WPI; 2002-224926/28.
XX
PT Library of expressible nucleic acids, useful for determining nucleic
PT acid function, comprises one or more adenoviral vectors capable of
PT transfecting a host cell with the nucleic acid -
XX
PS Example 18; Column 63; 111pp; English.
XX
CC The invention relates to a library (I) of a multitude of unique
CC expressible nucleic acids (NA), comprises a number of compartments
CC (II), each consisting of one or more adenoviral vectors (III)
CC comprising at least one unique NA of (I) in an aqueous medium, where
CC (III) is capable of introducing the NA into a host cell (IV), is
CC capable of expressing the product of the NA in (IV), and is deleted in
CC a portion of the adenoviral genome necessary for replication. Also
CC included is a method for producing the library. The library is useful for
CC determining the function of at least one nucleic acid that is present.
CC The library uses high throughput generation of recombinant adenoviral
CC vector libraries containing one or more sample nucleic acids, followed by
CC high throughput screening of the adenoviral vector libraries in a host to
CC alter the phenotype of the host as a means of assigning a function to
CC expression product(s) of the sample nucleic acids. The entire process
CC lends itself to automation especially when implemented in a 96-well or
CC other multi-well format. The high throughput screening, using a number of
CC different in vitro assays, provides a means of efficiently obtaining
CC functional information in a relatively short period of time. The
CC member(s) of the recombinant adenoviral libraries that exhibit or induce
CC a desired phenotype in a host in vitro or in situ are identified to
CC reduce the libraries to a manageable number of recombinant adenoviral
CC vectors or clones which can be tested in vitro in an animal model.
CC Furthermore, the methods produce RCA-free adenoviral libraries. RCA
CC (replication competent adenovirus) contamination throughout the libraries
CC could become a major obstacle, especially if libraries are continuously
CC amplified for use in multiple screening programs. Additionally, a further
CC advantage is minimisation of the number of steps involved in the process.
CC There is no requirement for cloning each individual adenovirus before use
CC in a high throughput screening program. Other systems include one or more
CC steps in E. coli to achieve homologous recombination for the various
CC adenoviral plasmids necessary for vector generation. The present
CC sequence is a PCR primer used in the construction of the adenoviral
CC vector library of the invention.
XX
SQ Sequence 27 BP; 3 A; 3 C; 13 G; 8 T; 0 other;

Query Match 69.5%; Score 13.2; DB 24; Length 27;
Best Local Similarity 83.3%; Pred. No. 5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2 GGTCTGCAGCGGGATGGT 19
           | |||| ||||||| |||
Db       8 GTTCTGGAGCGGGAGGGT 25
```

RESULT 14
AAQ97259/c
ID AAQ97259 standard; cDNA; 33 BP.
XX
AC AAQ97259;
XX
DT 28-DEC-1995 (first entry)
XX
DE ATF-2 5' bridging primer.
XX
KW Astrocyte-derived neurotrophic factor; ATF-1; neuron; GDNF;
KW primer; polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..17
FT /*tag= a
FT /note= "bases 1-17 corresp. to GDNF bases 95-111"
FT misc_feature 18..33
FT /*tag= b
FT /note= "bases 18-33 corresp. to GDNF bases 338-353"
XX
PN WO9517203-A1.
XX
PD 29-JUN-1995.
XX
PF 22-DEC-1994; 94WO-US14771.
XX
PR 20-DEC-1994; 94US-0359480.
PR 22-DEC-1993; 93US-0172327.
PR 18-JUL-1994; 94US-0275709.
XX
PA (UYNE-) UNIV NEW JERSEY.
XX
PI Black IB, Dreyfuss CF, Schaar DG;
XX
DR WPI; 1995-240472/31.
XX
PT New astrocyte-derived neurotrophic factor proteins - related nucleic
PT acid, vectors and transformed cells, useful for stimulating neuronal
PT cell survival and growth
XX
PS Example 1; Page 38; 107pp; English.
XX
CC The GDNF sequences deleted in human ATF-1 and ATF-2 cDNA clones
CC (AAQ97241-42, respectively) were analyzed by PCR using the bridging
CC primers given in AAQ97258-59. ATF mRNAs were expressed in substantia
CC nigra, caudate and putamen brain regions.
XX
SQ Sequence 33 BP; 6 A; 16 C; 7 G; 4 T; 0 other;

Query Match 69.5%; Score 13.2; DB 16; Length 33;
Best Local Similarity 83.3%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1 GGGTCTGCAGCGGGATGG 18
           ||||  |||||||||| ||
Db      28 GGGTTGGCAGCGGGAAGG 11
```

RESULT 15
AAT33615
ID AAT33615 standard; cDNA; 38 BP.
XX
AC AAT33615;
XX
DT 30-NOV-1996 (first entry)
XX
DE Murine VRF167 mRNA probe.
XX
KW VRF; vascular endothelial growth factor; VEGF; SOM175; neuron;
KW astroglial proliferation; probe; ss.
XX
OS Synthetic.
XX
PN WO9627007-A1.
XX
PD 06-SEP-1996.
XX
PF 22-FEB-1996; 96WO-AU00094.
XX
PR 22-DEC-1995; 95AU-0007274.
PR 02-MAR-1995; 95AU-0001457.
PR 20-NOV-1995; 95AU-0006647.
XX

PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
PI Weber G;
XX
DR WPI; 1996-412774/41.
XX
PT New growth factor related to vascular endothelial growth factor -
PT useful for inducing astroglial proliferation and promoting neuronal
PT survival
XX
PS Example 6; Page 27; 113pp; English.
XX
CC Oligonucleotide probes (AAT33615 and AAT33616) are complementary to
CC nucleotides found in the mRNA coding for alternatively spliced
CC murine VRF167 (see also AAT13810). They, and other probes (see also
CC AAT13811 and AAT33614) for VRF186 (see also AAT13809), were used to
CC examine expression of murine VRF in pre- and post-natal mice. The 4
CC probes gave identical hybridisation patterns in all tissues examined.
CC VRF expression was detected in the E14 mouse embryo, esp. in the heart
CC and nervous system. In E17 embryos, and in young adult mice,
CC expression was confined to the heart and brown fat tissue.
XX
SQ Sequence 38 BP; 6 A; 5 C; 18 G; 9 T; 0 other;

Query Match 69.5%; Score 13.2; DB 17; Length 38;
Best Local Similarity 83.3%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1 GGGTCTGCAGCGGGATGG 18
           ||| ||| || |||||||
Db       7 GGGGCTGGAGTGGGATGG 24
```

Search completed: November 28, 2002, 17:24:12
Job time : 177.575 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 16:42:34 ; Search time 1103.97 Seconds
(without alignments)
500.879 Million cell updates/sec

Title: US-09-719-737-9
Perfect score: 19
Sequence: 1 gggtctgcagcgggatggt 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	19	100.0	19	6	AX008655	AX008655 Sequence
	2	19	100.0	19	6	AX008656	AX008656 Sequence
	3	18	94.7	19	6	AX008657	AX008657 Sequence
	4	18	94.7	19	6	AX008658	AX008658 Sequence
	5	17	89.5	19	6	AX008662	AX008662 Sequence
	6	16	84.2	19	6	AX008659	AX008659 Sequence
c	7	14.2	74.7	34	6	E50113	E50113 DNA fragmen
c	8	13.2	69.5	43	6	A04394	A04394 Oligonucleo
	9	13.2	69.5	43	6	A04408	A04408 Oligonucleo
	10	13	68.4	19	6	AX008660	AX008660 Sequence
	11	12.8	67.4	50	6	AX199584	AX199584 Sequence
c	12	12.6	66.3	32	6	AR199663	AR199663 Sequence
c	13	12.6	66.3	33	6	AX058080	AX058080 Sequence
c	14	12.6	66.3	33	6	AX067827	AX067827 Sequence
c	15	12.6	66.3	33	6	AX078782	AX078782 Sequence
c	16	12.6	66.3	38	6	AR006787	AR006787 Sequence
c	17	12.6	66.3	38	6	AR135395	AR135395 Sequence
c	18	12.6	66.3	38	6	I71299	I71299 Sequence 37
c	19	12.6	66.3	41	6	AR096931	AR096931 Sequence
c	20	12.6	66.3	43	6	AR152008	AR152008 Sequence
c	21	12.6	66.3	43	6	AR161408	AR161408 Sequence
c	22	12.6	66.3	44	6	AR033897	AR033897 Sequence
c	23	12.6	66.3	44	6	AR175030	AR175030 Sequence
c	24	12.6	66.3	44	6	AX032462	AX032462 Sequence
c	25	12.6	66.3	44	6	AX057388	AX057388 Sequence
c	26	12.6	66.3	44	6	AX067833	AX067833 Sequence
	27	12.4	65.3	20	6	A45408	A45408 Sequence 78
	28	12.4	65.3	20	6	AR061213	AR061213 Sequence
	29	12.4	65.3	20	6	AR117659	AR117659 Sequence
	30	12.4	65.3	21	6	AX096151	AX096151 Sequence
	31	12.4	65.3	28	6	I11634	I11634 Sequence 19
	32	12.4	65.3	35	9	HUMD3E12M5	D17038 Human HepG2
	33	12.2	64.2	21	6	AX004671	AX004671 Sequence
	34	12.2	64.2	21	6	AX154148	AX154148 Sequence
c	35	12.2	64.2	21	6	AX327343	AX327343 Sequence
	36	12.2	64.2	25	6	AX393937	AX393937 Sequence
c	37	12.2	64.2	26	6	AX399113	AX399113 Sequence
	38	12.2	64.2	27	6	A07485	A07485 Nucleotide
c	39	12.2	64.2	31	6	AX249162	AX249162 Sequence
	40	12.2	64.2	31	6	E64737	E64737 Method for
	41	12.2	64.2	34	6	AR016403	AR016403 Sequence
	42	12.2	64.2	34	6	AR019261	AR019261 Sequence
c	43	12.2	64.2	34	6	I49868	I49868 Sequence 54
c	44	12.2	64.2	44	1	ECORRG06	K01112 E.coli 23S
	45	12.2	64.2	48	6	A07502	A07502 Nucleotide

ALIGNMENTS

RESULT 1
AX008655/c
LOCUS AX008655 19 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 8 from Patent WO9966037.
ACCESSION AX008655
VERSION AX008655.1 GI:9996179
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Renzi,P.
TITLE Antisense oligonucleotides for treating or preventing atopic diseases and neoplastic cell proliferation
JOURNAL Patent: WO 9966037-A 8 23-DEC-1999;

```
          RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Sense oligonucleotide for IL-3, IL-5 and GM-CSF"
BASE COUNT        4 a      10 c       3 g       2 t
ORIGIN

  Query Match           100.0%;  Score 19;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           ||||||||||||||||||||
Db      19 GGGTCTGCAGCGGGATGGT 1


RESULT 2
AX008656
LOCUS       AX008656                19 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 9 from Patent WO9966037.
ACCESSION   AX008656
VERSION     AX008656.1  GI:9996180
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Renzi,P.
  TITLE     Antisense oligonucleotides for treating or preventing atopic
            diseases and neoplastic cell proliferation
  JOURNAL   Patent: WO 9966037-A 9 23-DEC-1999;
            RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide inhibiting the common
                     subunit of IL-3, IL-5 and GM-CSF human receptor"
BASE COUNT        2 a      3 c      10 g      4 t
ORIGIN

  Query Match           100.0%;  Score 19;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           ||||||||||||||||||||
Db       1 GGGTCTGCAGCGGGATGGT 19


RESULT 3
AX008657
LOCUS       AX008657                19 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 10 from Patent WO9966037.
ACCESSION   AX008657
VERSION     AX008657.1  GI:9996181
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Renzi,P.
  TITLE     Antisense oligonucleotides for treating or preventing atopic
            diseases and neoplastic cell proliferation
  JOURNAL   Patent: WO 9966037-A 10 23-DEC-1999;
            RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide inhibiting the common
                     subunit of IL-3, IL-5 and GM-CSF human receptor"
BASE COUNT        2 a      3 c      9 g      5 t
ORIGIN

  Query Match           94.7%;  Score 18;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 GGTCTGCAGCGGGATGGT 19
           ||||||||||||||||||
Db       1 GGTCTGCAGCGGGATGGT 18


RESULT 4
AX008658
LOCUS       AX008658                19 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 11 from Patent WO9966037.
ACCESSION   AX008658
VERSION     AX008658.1  GI:9996182
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Renzi,P.
  TITLE     Antisense oligonucleotides for treating or preventing atopic
            diseases and neoplastic cell proliferation
  JOURNAL   Patent: WO 9966037-A 11 23-DEC-1999;
            RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide inhibiting the common
                     subunit of IL-3, IL-5 and GM-CSF human receptor"
BASE COUNT        3 a      3 c      10 g      3 t
ORIGIN

  Query Match           94.7%;  Score 18;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGG 18
           ||||||||||||||||||
Db       2 GGGTCTGCAGCGGGATGG 19


RESULT 5
AX008662
LOCUS       AX008662                19 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 15 from Patent WO9966037.
ACCESSION   AX008662
VERSION     AX008662.1  GI:9996186
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Renzi,P.
  TITLE     Antisense oligonucleotides for treating or preventing atopic
            diseases and neoplastic cell proliferation
  JOURNAL   Patent: WO 9966037-A 15 23-DEC-1999;
            RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide inhibiting the common
                     subunit of IL-3, IL-5 and GM-CSF human receptor"
BASE COUNT        2 a      3 c      8 g      6 t
ORIGIN

  Query Match           89.5%;  Score 17;  DB 6;  Length 19;
```

```
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GTCTGCAGCGGGATGGT 19
          |||||||||||||||||
Db      1 GTCTGCAGCGGGATGGT 17


RESULT 6
AX008659
LOCUS       AX008659                 19 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 12 from Patent WO9966037.
ACCESSION   AX008659
VERSION     AX008659.1  GI:9996183
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Renzi,P.
  TITLE     Antisense oligonucleotides for treating or preventing atopic
            diseases and neoplastic cell proliferation
  JOURNAL   Patent: WO 9966037-A 12 23-DEC-1999;
            RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide inhibiting the common
                     subunit of IL-3, IL-5 and GM-CSF human receptor"
BASE COUNT        3 a      4 c      9 g      3 t
ORIGIN

  Query Match             84.2%;  Score 16;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGTCTGCAGCGGGAT 16
          ||||||||||||||||
Db      4 GGGTCTGCAGCGGGAT 19


RESULT 7
E50113/c
LOCUS       E50113                   34 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  DNA fragment containing toluene monooxygenase gene, recombinant
            plasmid, transformed microorganism, process for decomposing
            halogenated aliphatic hydrocarbon and aromatic compound, and method
             for repairing environment by using the microorganism.
ACCESSION   E50113
VERSION     E50113.1  GI:18629391
KEYWORDS    JP 2000224994-A/2.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Yano,T., Nomoto,T. and Imamura,T.
  TITLE     DNA fragment containing toluene monooxygenase gene, recombinant
            plasmid, transformed microorganism, process for decomposing
            halogenated aliphatic hydrocarbon and aromatic compound, and method
            for repairing environment by using the microorganism
  JOURNAL   Patent: JP 2000224994-A 2 15-AUG-2000;
            CANON INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000224994-A/2
            PD   15-AUG-2000
            PF   03-DEC-1999 JP 1999345421
            PR
            PI   TETSUYA YANO,TAKESHI NOMOTO,TSUYOSHI IMAMURA
            PC   C12N15/09,A62D3/00,B01D53/70,B09C1/10,C02F3/34,C12N1/00, PC
            C12N1/21,
            PC   C12N9/04//(C12N1/21,C12R1:19),(C12N9/04,C12R1:19),C12N15/00,
            PC   B01D53/34,
            PC   B09B3/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .34
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        8 a      14 c      7 g      5 t
ORIGIN

  Query Match             74.7%;  Score 14.2;  DB 6;  Length 34;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+04;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 GGGTCTGCAGCGGGATGGT 19
          |||||||||| | |||||
Db     31 GGGTCTGCAGGGCCATGGT 13


RESULT 8
A04394/c
LOCUS       A04394                   43 bp    DNA     linear   PAT 29-APR-1993
DEFINITION  Oligonucleotide U5 for porcine growth hormone.
ACCESSION   A04394
VERSION     A04394.1  GI:344897
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT       11 a      15 c      13 g      4 t
ORIGIN

  Query Match             69.5%;  Score 13.2;  DB 6;  Length 43;
  Best Local Similarity   83.3%;  Pred. No. 9e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 GGTCTGCAGCGGGATGGT 19
          |||| ||  |||||||||
Db     18 GGTCGGCGCCGGGATGGT 1


RESULT 9
A04408
LOCUS       A04408                   43 bp    DNA     linear   PAT 29-APR-1993
DEFINITION  Oligonucleotide L5 for porcine growth hormone.
ACCESSION   A04408
VERSION     A04408.1  GI:344911
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT       10 a      10 c      15 g      8 t
ORIGIN

  Query Match             69.5%;  Score 13.2;  DB 6;  Length 43;
  Best Local Similarity   83.3%;  Pred. No. 9e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 GGTCTGCAGCGGGATGGT 19
          |||| ||  |||||||||
Db      8 GGTCGGCGCCGGGATGGT 25
```

```
RESULT 10
AX008660
LOCUS       AX008660                19 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 13 from Patent WO9966037.
ACCESSION   AX008660
VERSION     AX008660.1  GI:9996184
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Renzi,P.
  TITLE     Antisense oligonucleotides for treating or preventing atopic
            diseases and neoplastic cell proliferation
  JOURNAL   Patent: WO 9966037-A 13 23-DEC-1999;
            RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide inhibiting the common
                     subunit of IL-3, IL-5 and GM-CSF human receptor"
BASE COUNT        2 a      4 c      7 g      6 t
ORIGIN

  Query Match             68.4%;  Score 13;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 GCAGCGGGATGGT 19
           |||||||||||||
Db       1 GCAGCGGGATGGT 13


RESULT 11
AX199584
LOCUS       AX199584                50 bp    DNA     linear   PAT 29-AUG-2001
DEFINITION  Sequence 514 from Patent WO0151670.
ACCESSION   AX199584
VERSION     AX199584.1  GI:15390017
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Shimkets,R.A. and Leach,M.D.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0151670-A 514 19-JUL-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    25. .26
                     /note="Nucleotide deleted between bases 25 and 26
                     Accession number cg43951144"
     misc_feature    26
                     /note="2 of 2 allelic variants (513 is other entry)"
BASE COUNT       11 a     17 c     12 g     10 t
ORIGIN

  Query Match             67.4%;  Score 12.8;  DB 6;  Length 50;
  Best Local Similarity   87.5%;  Pred. No. 1.4e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGAT 16
           || |||||||||  |||
Db       8 GGATCTGCAGCGTGAT 23


RESULT 12
AR199663/c
LOCUS       AR199663                32 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 5 from patent US 6355479.
ACCESSION   AR199663
VERSION     AR199663.1  GI:20249737
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Webb,S.R., Winqvist,O., Karlsson,L., Jackson,M.R. and Peterson,P.A.
  TITLE     MHC class II antigen-presenting systems and methods for activating
            CD4+ T cells
  JOURNAL   Patent: US 6355479-A 5 12-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
BASE COUNT        7 a      12 c      5 g      8 t
ORIGIN

  Query Match             66.3%;  Score 12.6;  DB 6;  Length 32;
  Best Local Similarity   78.9%;  Pred. No. 1.8e+05;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           || ||||||| |  |||||
Db      29 GGATCTGCAGAGCCATGGT 11


RESULT 13
AX058080/c
LOCUS       AX058080                33 bp    DNA     linear   PAT 17-JAN-2001
DEFINITION  Sequence 9 from Patent WO0077188.
ACCESSION   AX058080
VERSION     AX058080.1  GI:12310660
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Audonnet,J.C., Bublot,M., Perez,J.M. and Charreyre,C.E.
  TITLE     Dna pcv vaccine
  JOURNAL   Patent: WO 0077188-A 9 21-DEC-2000;
            MERIAL (FR)
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
BASE COUNT        6 a      11 c     10 g      6 t
ORIGIN

  Query Match             66.3%;  Score 12.6;  DB 6;  Length 33;
  Best Local Similarity   78.9%;  Pred. No. 1.8e+05;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           || ||||||||   |||||
Db      31 GGTTCTGCAGCCACATGGT 13


RESULT 14
AX067827/c
LOCUS       AX067827                33 bp    DNA     linear   PAT 19-JAN-2001
DEFINITION  Sequence 64 from Patent WO0077043.
ACCESSION   AX067827
VERSION     AX067827.1  GI:12329705
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Fischer,L.J., barzu-le Roux,S. and Audonnet,J.C.
```

```
  TITLE     Dna vaccines for pets and sport animals
  JOURNAL   Patent: WO 0077043-A 64 21-DEC-2000;
            MERIAL (FR)
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucl otide"
BASE COUNT        6 a      11 c      10 g       6 t
ORIGIN

  Query Match             66.3%;  Score 12.6;  DB 6;  Length 33;
  Best Local Similarity   78.9%;  Pred. No. 1.8e+05;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           || ||||||||   |||||
Db      31 GGTTCTGCAGCCACATGGT 13


RESULT 15
AX078782/c
LOCUS       AX078782                 33 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 20 from Patent WO0105934.
ACCESSION   AX078782
VERSION     AX078782.1  GI:13158399
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Audonnet,J.C., Baudu,P.G. and Brunet,S.C.
  TITLE     Feline calicivirus genes and vaccines, in particular recombined
            vaccines
  JOURNAL   Patent: WO 0105934-A 20 25-JAN-2001;
            MERIAL (FR)
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
BASE COUNT        6 a      11 c      10 g       6 t
ORIGIN

  Query Match             66.3%;  Score 12.6;  DB 6;  Length 33;
  Best Local Similarity   78.9%;  Pred. No. 1.8e+05;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGTCTGCAGCGGGATGGT 19
           || ||||||||   |||||
Db      31 GGTTCTGCAGCCACATGGT 13


Search completed: November 28, 2002, 18:20:38
Job time : 1105.97 secs
```

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 17:10:34 ; Search time 1372.59 Seconds
(without alignments)
224.186 Million cell updates/sec

Title: US-09-719-737-18
Perfect score: 19
Sequence: 1 ctgggccatcagtgctctg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	12.4	65.3	38	17	AZ834919	AZ834919 2M0117D21
	2	12.2	64.2	29	17	TA59B05Q	AL456550 T. brucei
	3	12	63.2	31	12	BF181705	BF181705 601805518
c	4	12	63.2	38	17	BH792093	BH792093 SALK_0626
	5	12	63.2	49	17	AZ472469	AZ472469 1M0287P09
c	6	11.8	62.1	35	13	BJ084423	BJ084423 BJ084423
c	7	11.8	62.1	36	17	AL762128	AL762128 Arabidops
	8	11.8	62.1	37	17	AZ384612	AZ384612 1M0142O08
	9	11.8	62.1	44	17	BH000259	BH000259 2M0288A03
c	10	11.8	62.1	45	17	AZ309922	AZ309922 1M0017C23
c	11	11.8	62.1	48	17	BH791856	BH791856 SALK_0618
	12	11.6	61.1	33	17	AZ391565	AZ391565 1M0153F16
	13	11.6	61.1	35	12	BF793800	BF793800 602254477
	14	11.6	61.1	40	17	AZ807388	AZ807388 2M0070O10
	15	11.6	61.1	41	17	AZ774224	AZ774224 2M0003E19
c	16	11.4	60.0	39	17	AZ829271	AZ829271 2M0106P15
	17	11.4	60.0	41	17	AZ437628	AZ437628 1M0226F08
c	18	11.4	60.0	44	10	AV843723	AV843723 AV843723
	19	11.4	60.0	48	17	AZ602280	AZ602280 1M0420P21
	20	11.2	58.9	31	9	AA181661	AA181661 zp55c05.r
	21	11.2	58.9	31	13	BI154945	BI154945 602902750
	22	11.2	58.9	33	13	BI103577	BI103577 602888724
	23	11.2	58.9	34	9	AA109657	AA109657 mp33h12.r
	24	11.2	58.9	49	9	AA691710	AA691710 vu16d04.r
	25	11	57.9	25	17	AZ648037	AZ648037 1M0514C23
	26	11	57.9	30	17	AZ949156	AZ949156 2M0212D01
	27	11	57.9	32	10	AV834034	AV834034 AV834034
	28	11	57.9	32	10	AV956830	AV956830 AV956830
	29	11	57.9	32	17	AZ441593	AZ441593 1M0233M24
	30	11	57.9	32	17	AZ600248	AZ600248 1M0418D11
	31	11	57.9	32	17	AZ816444	AZ816444 2M0085M12
	32	11	57.9	34	17	AZ482003	AZ482003 1M0306D16
c	33	11	57.9	35	17	AZ581423	AZ581423 1M0370L07
	34	11	57.9	35	17	AZ860292	AZ860292 2M0166B10
	35	11	57.9	35	17	BH128269	BH128269 G-2p13.f
c	36	11	57.9	43	9	AI496922	AI496922 fb53a03.x
	37	11	57.9	43	17	AZ834960	AZ834960 2M0117L19
	38	11	57.9	44	13	BJ033250	BJ033250 BJ033250
	39	11	57.9	44	17	AZ662473	AZ662473 1M0541A10
c	40	11	57.9	45	17	AZ839967	AZ839967 2M0136L13
	41	11	57.9	46	9	AA652871	AA652871 ns75e09.s
	42	11	57.9	47	17	AZ481505	AZ481505 1M0303J17
c	43	11	57.9	49	9	AI744224	AI744224 tr07g01.x
c	44	11	57.9	50	9	AU102583	AU102583 AU102583
	45	11	57.9	50	9	AU105201	AU105201 AU105201

ALIGNMENTS

RESULT 1
AZ834919/c
LOCUS AZ834919 38 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0117D21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0117D21 R, DNA sequence.
ACCESSION AZ834919
VERSION AZ834919.1 GI:13004827
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 38)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss,
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

```
            Plate: 0117  row: D  column: 21
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 38.
FEATURES              Location/Qualifiers
     source           1. .38
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0117D21"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT        15 a      10 c       7 g       6 t
ORIGIN

  Query Match             65.3%;  Score 12.4;  DB 17;  Length 38;
  Best Local Similarity   92.9%;  Pred. No. 4e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 TGGGCCATCAGTGC 15
           |||| |||||||||
Db      30 TGGGTCATCAGTGC 17


RESULT 2
TA59B05Q
LOCUS       TA59B05Q                  29 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 59b05, reverse sequence,
            genomic survey sequence.
ACCESSION   AL456550
VERSION     AL456550.1  GI:11858271
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES              Location/Qualifiers
     source           1. .29
                      /organism="Trypanosoma brucei"
                      /strain="TREU927"
                      /db_xref="taxon:5691"
                      /clone="59b05"
BASE COUNT        5 a      11 c       6 g       7 t
ORIGIN

  Query Match             64.2%;  Score 12.2;  DB 17;  Length 29;
  Best Local Similarity   82.4%;  Pred. No. 4.3e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTC 17
           |||| || |||| ||||
Db      13 CTGGTCCCTCAGGGCTC 29


RESULT 3
BF181705
LOCUS       BF181705                  31 bp    mRNA    linear   EST 31-OCT-2000
DEFINITION  601805518F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4036180 5',
            mRNA sequence.
ACCESSION   BF181705
VERSION     BF181705.1  GI:11059847
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9311  row: d  column: 05
            High quality sequence stop: 31.
FEATURES              Location/Qualifiers
     source           1. .31
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:4036180"
                      /clone_lib="NCI_CGAP_Mam5"
                      /tissue_type="tumor, gross tissue"
                      /dev_stage="7 months"
                      /lab_host="DH10B"
                      /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Library constructed by Life Technologies. Investigators
                      providing samples: Lothar Hennighausen/Robin Humphreys,
                      NIH"
BASE COUNT        5 a      10 c      10 g       6 t
ORIGIN

  Query Match             63.2%;  Score 12;  DB 12;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAG 12
           ||||||||||||
```

Db 3 CTGGGCCATCAG 14

RESULT 4
BH792093/c
LOCUS BH792093 38 bp DNA linear GSS 02-APR-2002
DEFINITION SALK_062674.45.30.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_062674.45.30.x, DNA sequence.
ACCESSION BH792093
VERSION BH792093.1 GI:19888485
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 38)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P. , Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At5g05390.
Class: TDNA tagged.
FEATURES Location/Qualifiers
source 1. .38
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_062674.45.30.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT 12 a 7 c 13 g 6 t
ORIGIN

Query Match 63.2%; Score 12; DB 17; Length 38;
Best Local Similarity 100.0%; Pred. No. 6.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGGGCCATCAG 12
||||||||||||
Db 34 CTGGGCCATCAG 23

RESULT 5
AZ472469
LOCUS AZ472469 49 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0287P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0287P09 R, DNA sequence.
ACCESSION AZ472469
VERSION AZ472469.1 GI:10630594
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 49)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0287 row: P column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 49.
FEATURES Location/Qualifiers
source 1. .49
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0287P09"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 10 a 11 c 15 g 13 t
ORIGIN

Query Match 63.2%; Score 12; DB 17; Length 49;
Best Local Similarity 100.0%; Pred. No. 7.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGGCCATCAGTG 14
||||||||||||
Db 29 GGGCCATCAGTG 40

RESULT 6
BJ084423/c
LOCUS BJ084423 35 bp mRNA linear EST 12-DEC-2001
DEFINITION BJ084423 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL089c18 3', mRNA sequence.
ACCESSION BJ084423
VERSION BJ084423.1 GI:17579964
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 35)

```
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
            ,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="Xenopus laevis"
                     /db_xref="taxon:8355"
                     /clone="XL089c18"
                     /clone_lib="NIBB Mochii normalized Xenopus tailbud
                     library"
                     /tissue_type="whole embryo"
                     /dev_stage="stage 25"
                     /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
                     were oligo-dT primed and directionally cloned. Staging
                     according to  Nieuwkoop and Faber. Library is subtracted
                     and was constructed by N. Garrett  and A.M. Zorn,
                     (Wellcome/CRC Institute). "
BASE COUNT        9 a      6 c      9 g     10 t      1 others
ORIGIN

  Query Match             62.1%;  Score 11.8;  DB 13;  Length 35;
  Best Local Similarity   86.7%;  Pred. No. 7.3e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4 GGCCATCAGTGCTCT 18
           ||| ||||| |||||
Db      29 GGCAATCAGAGCTCT 15


RESULT 7
AL762128/c
LOCUS       AL762128                 36 bp    DNA     linear   GSS 18-JUN-2002
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-021B05-013692,
            genomic survey sequence.
ACCESSION   AL762128
VERSION     AL762128.1  GI:21506683
KEYWORDS    GSS.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 36)
  AUTHORS   Rosso,M., Li,Y., Strizhov,N. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion within the locus defined by clone t5e7. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-021B05-013692"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC106. The lines contain one or more T-DNA
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thalaina nuclear genome sequence were
                     processed for submission. T-DNA derived sequences were
                     removed"
BASE COUNT        7 a      13 c      7 g      9 t
ORIGIN

  Query Match             62.1%;  Score 11.8;  DB 17;  Length 36;
  Best Local Similarity   86.7%;  Pred. No. 7.5e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 TGGGCCATCAGTGCT 16
             ||||  |||||||||
Db      31 TGGGGAATCAGTGCT 17


RESULT 8
AZ384612 .
LOCUS       AZ384612                 37 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0142O08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0142O08 R, DNA sequence.
ACCESSION   AZ384612
VERSION     AZ384612.1  GI:10498312
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0142  row: O  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 37.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0142O08"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
```

Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 10 c 14 g 9 t
ORIGIN

Query Match 62.1%; Score 11.8; DB 17; Length 37;
Best Local Similarity 86.7%; Pred. No. 7.6e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy      1 CTGGGCCATCAGTGC 15
          ||||||| ||| |||
Db     12 CTGGGCCCTCATTGC 26
```

RESULT 9
BH000259
LOCUS BH000259 44 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0288A03F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0288A03 F, DNA sequence.
ACCESSION BH000259
VERSION BH000259.1 GI:13871485
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 44)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0288 row: A column: 03
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 44.
FEATURES Location/Qualifiers
source 1. .44
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0288A03"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 14 a 8 c 10 g 12 t
ORIGIN

Query Match 62.1%; Score 11.8; DB 17; Length 44;
Best Local Similarity 86.7%; Pred. No. 8.3e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy      5 GCCATCAGTGCTCTG 19
          || |||| |||||||
Db     22 GCTATCAATGCTCTG 36
```

RESULT 10
AZ309922/c
LOCUS AZ309922 45 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0017C23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0017C23 F, DNA sequence.
ACCESSION AZ309922
VERSION AZ309922.1 GI:10351397
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 45)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0017 row: C column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 45.
FEATURES Location/Qualifiers
source 1. .45
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0017C23"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 19 a 14 c 3 g 9 t
ORIGIN

Query Match 62.1%; Score 11.8; DB 17; Length 45;
Best Local Similarity 86.7%; Pred. No. 8.4e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       2 TGGGCCATCAGTGCT 16
           ||| |||||||||  |
Db      28 TGGTCCATCAGTGTT 14
```

RESULT 11
BH791856/c
LOCUS BH791856 48 bp DNA linear GSS 02-APR-2002
DEFINITION SALK_061836.50.60.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_061836.50.60.x, DNA sequence.
ACCESSION BH791856
VERSION BH791856.1 GI:19886151
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 48)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At5g14310.
Class: TDNA tagged.
FEATURES Location/Qualifiers
source 1. .48
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_061836.50.60.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 15 a 9 c 12 g 12 t
ORIGIN

Query Match 62.1%; Score 11.8; DB 17; Length 48;
Best Local Similarity 86.7%; Pred. No. 8.7e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       4 GGCCATCAGTGCTCT 18
           |||||| ||| ||||
Db      18 GGCCATGAGTTCTCT 4
```

RESULT 12
AZ391565
LOCUS AZ391565 33 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0153F16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0153F16 R, DNA sequence.
ACCESSION AZ391565
VERSION AZ391565.1 GI:10506608
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 33)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0153 row: F column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 33.
FEATURES Location/Qualifiers
source 1. .33
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0153F16"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
BASE COUNT        5 a      8 c      7 g     13 t
ORIGIN

  Query Match             61.1%;  Score 11.6;  DB 17;  Length 33;
  Best Local Similarity   77.8%;  Pred. No. 8.8e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 TGGGCCATCAGTGCTCTG 19
          |||| ||||| | || ||
Db     12 TGGGACATCATTTCTTTG 29


RESULT 13
BF793800
LOCUS       BF793800                 35 bp    mRNA    linear   EST 12-JAN-2001
DEFINITION  602254477F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4346610 5',
            mRNA sequence.
ACCESSION   BF793800
VERSION     BF793800.1  GI:12098863
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9968  row: j  column: 19
            High quality sequence stop: 35.
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4346610"
                     /clone_lib="NIH_MGC_84"
                     /tissue_type="adrenal cortex carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
                     NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
                     primed. Average insert size 1.229 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT        3 a     15 c      8 g      9 t
ORIGIN

  Query Match             61.1%;  Score 11.6;  DB 12;  Length 35;
  Best Local Similarity   77.8%;  Pred. No. 9.1e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 CTGGGCCATCAGTGCTCT 18
          |||||||| ||  || ||
Db     16 CTGGGCCACCATAGCCCT 33


RESULT 14
AZ807388
LOCUS       AZ807388                 40 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0070O10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0070O10 F, DNA sequence.
ACCESSION   AZ807388
VERSION     AZ807388.1  GI:12971685
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0070  row: O  column: 10
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 40.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0070O10"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        6 a      6 c     17 g     11 t
ORIGIN

  Query Match             61.1%;  Score 11.6;  DB 17;  Length 40;
  Best Local Similarity   77.8%;  Pred. No. 9.8e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 CTGGGCCATCAGTGCTCT 18
          ||||| ||| |||| | |
Db     13 CTGGGGCATGAGTGTTTT 30


RESULT 15
AZ774224
LOCUS       AZ774224                 41 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0003E19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0003E19 F, DNA sequence.
ACCESSION   AZ774224
VERSION     AZ774224.1  GI:12899427
KEYWORDS    GSS.
SOURCE      house mouse.
```

```
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0003  row: E  column: 19
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 41.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0003E19"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        6 a      9 c     11 g     15 t
ORIGIN

  Query Match             61.1%;  Score 11.6;  DB 17;  Length 41;
  Best Local Similarity   77.8%;  Pred. No. 9.9e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCT 18
           || |  |||||||| |||
Db      16 CTTGAGCATCAGTGGTCT 33


Search completed: November 28, 2002, 19:30:47
Job time : 1375.59 secs
```

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 17:15:39 ; Search time 39.9655 Seconds
(without alignments)
183.088 Million cell updates/sec

Title: US-09-719-737-18
Perfect score: 19
Sequence: 1 ctgggccatcagtgctctg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 341543 seqs, 192557720 residues

Total number of hits satisfying chosen parameters: 177872

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	13	68.4	36	10	US-09-504-231A-1780	Sequence 1780, Ap
c	2	13	68.4	36	10	US-09-274-553D-1780	Sequence 1780, Ap
c	3	12.8	67.4	17	10	US-09-866-108-6582	Sequence 6582, Ap
c	4	12.8	67.4	17	10	US-09-866-108-6583	Sequence 6583, Ap
c	5	12.8	67.4	25	10	US-09-795-232-4	Sequence 4, Appli
c	6	12.8	67.4	25	10	US-09-866-108-11474	Sequence 11474, A
c	7	12.8	67.4	25	10	US-09-866-108-11475	Sequence 11475, A
c	8	12.8	67.4	25	10	US-09-866-108-11476	Sequence 11476, A
c	9	12.8	67.4	25	10	US-09-866-108-11477	Sequence 11477, A
c	10	12.8	67.4	25	10	US-09-866-108-11478	Sequence 11478, A
c	11	12.8	67.4	25	10	US-09-866-108-11479	Sequence 11479, A
c	12	12.8	67.4	25	10	US-09-866-108-11480	Sequence 11480, A
c	13	12.8	67.4	25	10	US-09-866-108-11481	Sequence 11481, A
c	14	12.8	67.4	25	10	US-09-866-108-11482	Sequence 11482, A
c	15	12.8	67.4	25	10	US-09-866-108-11483	Sequence 11483, A
	16	12.6	66.3	43	10	US-09-766-378A-2	Sequence 2, Appli
	17	12.6	66.3	44	10	US-09-848-164-40	Sequence 40, Appl
	18	12.4	65.3	17	9	US-09-872-462-249	Sequence 249, App
	19	12.4	65.3	17	9	US-09-872-462-250	Sequence 250, App
	20	12.4	65.3	17	9	US-09-872-462-251	Sequence 251, App
	21	12.4	65.3	17	9	US-09-872-462-252	Sequence 252, App
c	22	12.4	65.3	20	10	US-09-820-339A-22	Sequence 22, Appl
	23	12.4	65.3	25	9	US-09-872-462-460	Sequence 460, App
	24	12.4	65.3	25	9	US-09-872-462-461	Sequence 461, App
	25	12.4	65.3	25	9	US-09-872-462-462	Sequence 462, App
	26	12.4	65.3	25	9	US-09-872-462-463	Sequence 463, App
	27	12.4	65.3	25	9	US-09-872-462-464	Sequence 464, App
	28	12.4	65.3	25	9	US-09-872-462-465	Sequence 465, App
	29	12.4	65.3	25	9	US-09-872-462-466	Sequence 466, App
	30	12.4	65.3	25	9	US-09-872-462-467	Sequence 467, App
	31	12.4	65.3	30	10	US-09-898-541-24	Sequence 24, Appl
c	32	12.2	64.2	20	10	US-09-854-883-193	Sequence 193, App
c	33	12.2	64.2	31	10	US-09-801-274-1400	Sequence 1400, Ap
	34	12	63.2	17	9	US-09-872-462-253	Sequence 253, App
	35	12	63.2	17	9	US-09-872-462-254	Sequence 254, App
	36	12	63.2	31	10	US-09-801-274-1721	Sequence 1721, Ap
	37	12	63.2	39	10	US-09-894-633A-7	Sequence 7, Appli
c	38	11.8	62.1	17	10	US-09-866-108-6581	Sequence 6581, Ap
c	39	11.8	62.1	17	10	US-09-866-108-6584	Sequence 6584, Ap
	40	11.8	62.1	18	9	US-09-905-291A-387	Sequence 387, App
	41	11.8	62.1	18	10	US-09-909-320-387	Sequence 387, App
	42	11.8	62.1	18	10	US-09-909-088B-387	Sequence 387, App
c	43	11.8	62.1	25	10	US-09-866-108-11473	Sequence 11473, A
c	44	11.8	62.1	25	10	US-09-866-108-11484	Sequence 11484, A
c	45	11.6	61.1	30	9	US-09-898-234-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-504-231A-1780/c
; Sequence 1780, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS REL
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1780
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Mo
US-09-504-231A-1780

Query Match 68.4%; Score 13; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       7 CATCAGTGCTCTG 19
           |||||||||||||
Db      13 CATCAGTGCTCTG 1
```

```
RESULT 2
US-09-274-553D-1780/c
; Sequence 1780, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
;  APPLICANT: Blatt, Lawrence
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Roberts, Beth
;  APPLICANT:  Pavco, Pamela
;  APPLICANT:  Macejak, Dennis
;  TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
;  TITLE OF INVENTION:  HEPATITIS C VIRUS INFECTION
;  FILE REFERENCE: rpi 247/282
;  CURRENT APPLICATION NUMBER: US/09/274,553D
;  CURRENT FILING DATE:  1999-03-23
;  PRIOR APPLICATION NUMBER: 09/257,608
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 60/100,842
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/083,217
;  PRIOR FILING DATE: 1998-04-27
;  NUMBER OF SEQ ID NOS: 3148
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1780
;   LENGTH: 36
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid Molec
US-09-274-553D-1780

  Query Match             68.4%;  Score 13;  DB 10;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 CATCAGTGCTCTG 19
           |||||||||||||
Db      13 CATCAGTGCTCTG 1


RESULT 3
US-09-866-108-6582/c
; Sequence 6582, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6582
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-6582

  Query Match             67.4%;  Score 12.8;  DB 10;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 8.1e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCT 16
           |||| || ||||||||
Db      17 CTGGACCCTCAGTGCT 2


RESULT 4
US-09-866-108-6583/c
; Sequence 6583, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
```

```
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6583
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-6583

  Query Match             67.4%;  Score 12.8;  DB 10;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 8.1e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 CTGGGCCATCAGTGCT 16
          |||| || ||||||||
Db     16 CTGGACCCTCAGTGCT 1


RESULT 5
US-09-795-232-4/c
; Sequence 4, Application US/09795232
; Patent No. US20010012627A1
; GENERAL INFORMATION:
;  APPLICANT:  Anthony M. Brown
;  APPLICANT:  Conrad Gerald Chapman
;  APPLICANT:  Israel Simon Gloger
;  APPLICANT:  Joanne Rachel Evans
;  APPLICANT:  William Cairns
;  APPLICANT:  Hugh Jonathan Herdon
;  TITLE OF INVENTION:  NOVEL COMPOUNDS
;  FILE REFERENCE:  GP-30176-D1
;  CURRENT APPLICATION NUMBER: US/09/795,232
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER:  09/182,728
;  PRIOR FILING DATE:  1998-10-29
;  PRIOR APPLICATION NUMBER:  9818890.7
;  PRIOR FILING DATE:  1998-08-28
;  NUMBER OF SEQ ID NOS:  6
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-09-795-232-4

  Query Match             67.4%;  Score 12.8;  DB 10;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 CTGGGCCATCAGTGCT 16
          |||||| ||||||||
Db     21 CTGGGCACTCAGTGCT 6


RESULT 6
US-09-866-108-11474/c
; Sequence 11474, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 11474
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-11474

  Query Match             67.4%;  Score 12.8;  DB 10;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 CTGGGCCATCAGTGCT 16
          |||| || ||||||||
Db     25 CTGGACCCTCAGTGCT 10


RESULT 7
US-09-866-108-11475/c
; Sequence 11475, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
```

```
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 11475
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-11475

  Query Match             67.4%;  Score 12.8;  DB 10;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCT 16
           |||| || ||||||||
Db      24 CTGGACCCTCAGTGCT 9


RESULT 8
US-09-866-108-11476/c
; Sequence 11476, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 11476
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-11476

  Query Match             67.4%;  Score 12.8;  DB 10;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCT 16
           |||| || ||||||||
Db      23 CTGGACCCTCAGTGCT 8


RESULT 9
US-09-866-108-11477/c
; Sequence 11477, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
```

```
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 11477
;    LENGTH: 25
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-866-108-11477

  Query Match             67.4%;  Score 12.8;  DB 10;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCT 16
           |||| || ||||||||
Db      22 CTGGACCCTCAGTGCT 7


RESULT 10
US-09-866-108-11478/c
; Sequence 11478, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 11478
;    LENGTH: 25
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-866-108-11478

  Query Match             67.4%;  Score 12.8;  DB 10;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCT 16
           |||| || ||||||||
Db      21 CTGGACCCTCAGTGCT 6


RESULT 11
US-09-866-108-11479/c
; Sequence 11479, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 11479
;    LENGTH: 25
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-866-108-11479

  Query Match             67.4%;  Score 12.8;  DB 10;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCT 16
           |||| || ||||||||
Db      20 CTGGACCCTCAGTGCT 5


RESULT 12
US-09-866-108-11480/c
; Sequence 11480, Application US/09866108
; Patent No. US20020048800A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 11480
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-11480

  Query Match             67.4%;  Score 12.8;  DB 10;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCT 16
           |||| || ||||||||
Db      19 CTGGACCCTCAGTGCT 4


RESULT 13
US-09-866-108-11481/c
; Sequence 11481, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 11481
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-11481

  Query Match             67.4%;  Score 12.8;  DB 10;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCT 16
           |||| || ||||||||
Db      18 CTGGACCCTCAGTGCT 3


RESULT 14
US-09-866-108-11482/c
; Sequence 11482, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
```

```
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 11482
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-11482

  Query Match             67.4%;  Score 12.8;  DB 10;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCT 16
           |||| || ||||||||
Db      17 CTGGACCCTCAGTGCT 2


RESULT 15
US-09-866-108-11483/c
; Sequence 11483, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 11483
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-11483

  Query Match             67.4%;  Score 12.8;  DB 10;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCT 16
           |||| || ||||||||
Db      16 CTGGACCCTCAGTGCT 1


Search completed: November 28, 2002, 19:35:04
Job time : 39.9655 secs
```

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 17:12:29 ; Search time 38.3276 Seconds
(without alignments)
152.028 Million cell updates/sec

Title: US-09-719-737-18
Perfect score: 19
Sequence: 1 ctgggccatcagtgctctg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	15.8	83.2	45	2	US-08-687-355A-14	Sequence 14, Appl
c	2	15.8	83.2	45	4	US-09-407-367-14	Sequence 14, Appl
	3	14.8	77.9	45	2	US-08-687-355A-13	Sequence 13, Appl
	4	14.8	77.9	45	4	US-09-407-367-13	Sequence 13, Appl
	5	14.4	75.8	20	1	US-08-742-023-15	Sequence 15, Appl
	6	14.4	75.8	20	3	US-08-968-505-15	Sequence 15, Appl
c	7	13.2	69.5	33	3	US-09-233-506-11	Sequence 11, Appl
c	8	13	68.4	27	4	US-08-584-040-4815	Sequence 4815, Ap
c	9	12.8	67.4	25	4	US-09-182-728A-4	Sequence 4, Appli
c	10	12.8	67.4	25	4	US-09-795-232-4	Sequence 4, Appli
	11	12.6	66.3	43	4	US-08-960-190A-2	Sequence 2, Appli
	12	12.6	66.3	44	2	US-08-596-387B-40	Sequence 40, Appl
	13	12.6	66.3	44	4	US-09-067-615-40	Sequence 40, Appl
	14	12.6	66.3	44	5	PCT-US95-09816A-40	Sequence 40, Appl
c	15	12.4	65.3	18	3	US-08-773-731A-12	Sequence 12, Appl
	16	12.4	65.3	30	4	US-09-230-199-24	Sequence 24, Appl
	17	12.4	65.3	31	1	US-08-390-850-222	Sequence 222, App
	18	12.4	65.3	31	1	US-08-390-850-223	Sequence 223, App
	19	12.4	65.3	31	1	US-08-390-850-224	Sequence 224, App
	20	12.4	65.3	31	1	US-08-435-634-222	Sequence 222, App
	21	12.4	65.3	31	1	US-08-435-634-223	Sequence 223, App
	22	12.4	65.3	31	1	US-08-435-634-224	Sequence 224, App
	23	12.4	65.3	31	2	US-08-859-998-167	Sequence 167, App
	24	12.4	65.3	31	4	US-09-225-928-167	Sequence 167, App
	25	12.4	65.3	40	4	US-09-485-737B-35	Sequence 35, Appl
c	26	12.2	64.2	20	4	US-09-487-368A-193	Sequence 193, App
c	27	12.2	64.2	36	4	US-09-101-126-13	Sequence 13, Appl
c	28	12.2	64.2	45	2	US-08-944-982-1	Sequence 1, Appli
	29	12	63.2	20	4	US-09-429-322-61	Sequence 61, Appl
	30	12	63.2	21	3	US-09-009-913-19	Sequence 19, Appl
c	31	12	63.2	27	4	US-08-584-040-1443	Sequence 1443, Ap
c	32	12	63.2	27	4	US-08-584-040-3326	Sequence 3326, Ap
c	33	12	63.2	27	4	US-08-584-040-5279	Sequence 5279, Ap
c	34	12	63.2	36	1	US-08-291-932A-568	Sequence 568, App
	35	11.8	62.1	20	2	US-08-117-952-476	Sequence 476, App
	36	11.8	62.1	27	3	US-08-513-974B-121	Sequence 121, App
c	37	11.8	62.1	36	1	US-08-484-686B-18	Sequence 18, Appl
c	38	11.8	62.1	36	4	US-08-463-160B-18	Sequence 18, Appl
c	39	11.8	62.1	45	1	US-08-171-389-257	Sequence 257, App
c	40	11.8	62.1	45	1	US-08-167-939A-13	Sequence 13, Appl
c	41	11.8	62.1	45	1	US-08-123-936-257	Sequence 257, App
c	42	11.8	62.1	45	1	US-08-567-538-13	Sequence 13, Appl
c	43	11.8	62.1	45	2	US-08-475-228A-257	Sequence 257, App
c	44	11.8	62.1	45	3	US-08-482-080A-257	Sequence 257, App
c	45	11.8	62.1	45	4	US-09-354-947-257	Sequence 257, App

ALIGNMENTS

```
RESULT 1
US-08-687-355A-14/c
; Sequence 14, Application US/08687355A
; Patent No. 5989834
;  GENERAL INFORMATION:
;    APPLICANT:  Synaptic Pharmaceutical Corporation
;    TITLE OF INVENTION:  NUCLEIC ACID ENCODING  NEUROPEPTIDE
;    TITLE OF INVENTION:  Y/PEPTIDE YY (Y2) RECEPTORS AND USES THEREOF
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/687,355A
;      FILING DATE:  No. 5989834ember 26, 1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  44742-A-PCT/JPW/MAT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-391-0525
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-687-355A-14

  Query Match             83.2%;  Score 15.8;  DB 2;  Length 45;
  Best Local Similarity   89.5%;  Pred. No. 16;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCTG 19
           ||||| ||||||||| |||
Db      43 CTGGGGCATCAGTGCCCTG 25
```

```
RESULT 2
US-09-407-367-14/c
; Sequence 14, Application US/09407367
; Patent No. 6420532
;  GENERAL INFORMATION:
;    APPLICANT:  Christophe P.G. Gerald, et al.
;    TITLE OF INVENTION:  METHOD OF OBTAINING COMPOSITIONS COMPRISING Y2 SPECIFIC COMPO
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/407,367
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  44742-AA-PCT-US/JPW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-391-0525
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-09-407-367-14

  Query Match             83.2%;  Score 15.8;  DB 4;  Length 45;
  Best Local Similarity   89.5%;  Pred. No. 16;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCTG 19
           ||||| |||||||||| |||
Db      43 CTGGGGCATCAGTGCCCTG 25


RESULT 3
US-08-687-355A-13
; Sequence 13, Application US/08687355A
; Patent No. 5989834
;  GENERAL INFORMATION:
;    APPLICANT:  Synaptic Pharmaceutical Corporation
;    TITLE OF INVENTION:  NUCLEIC ACID ENCODING  NEUROPEPTIDE
;    TITLE OF INVENTION:  Y/PEPTIDE YY (Y2) RECEPTORS AND USES THEREOF
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/687,355A
;      FILING DATE:  No. 5989834ember 26, 1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  44742-A-PCT/JPW/MAT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-391-0525
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-687-355A-13

  Query Match             77.9%;  Score 14.8;  DB 2;  Length 45;
  Best Local Similarity   88.9%;  Pred. No. 53;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCT 18
           ||||| |||||||||| ||
Db      28 CTGGGGCATCAGTGCCCT 45


RESULT 4
US-09-407-367-13
; Sequence 13, Application US/09407367
; Patent No. 6420532
;  GENERAL INFORMATION:
;    APPLICANT:  Christophe P.G. Gerald, et al.
;    TITLE OF INVENTION:  METHOD OF OBTAINING COMPOSITIONS COMPRISING Y2 SPECIFIC COM
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/407,367
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  44742-AA-PCT-US/JPW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-391-0525
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-09-407-367-13
```

```
  Query Match            77.9%;  Score 14.8;  DB 4;  Length 45;
  Best Local Similarity  88.9%;  Pred. No. 53;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCT 18
           ||||| |||||||||| ||
Db      28 CTGGGGCATCAGTGCCCT 45


RESULT 5
US-08-742-023-15
; Sequence 15, Application US/08742023
; Patent No. 5800997
;  GENERAL INFORMATION:
;    APPLICANT:  Beck, James J.
;    TITLE OF INVENTION:  Detection of Maize Fungal Pathogens
;    TITLE OF INVENTION:  Using the Polymerase Chain Reaction
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CIBA-GEIGY Corporation
;      STREET:  520 White Plains Road, P.O. Box 2005
;      CITY:  Tarrytown
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10591
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/742,023
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meigs, J. Timothy
;      REGISTRATION NUMBER:  38,241
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919) 541-8587
;      TELEFAX:  (919) 541-8689
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "primer JB586"
US-08-742-023-15

  Query Match            75.8%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity  93.8%;  Pred. No. 76;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 GGCCATCAGTGCTCTG 19
           ||| ||||||||||||
Db       2 GGCAATCAGTGCTCTG 17


RESULT 6
US-08-968-505-15
; Sequence 15, Application US/08968505
; Patent No. 6071698
;  GENERAL INFORMATION:
;    APPLICANT:  Beck, James J.
;    TITLE OF INVENTION:  Detection of Maize Fungal Pathogens
;    TITLE OF INVENTION:  Using the Polymerase Chain Reaction
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CIBA-GEIGY Corporation
;      STREET:  520 White Plains Road, P.O. Box 2005
;      CITY:  Tarrytown
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10591
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/968,505
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/742,023
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meigs, J. Timothy
;      REGISTRATION NUMBER:  38,241
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919) 541-8587
;      TELEFAX:  (919) 541-8689
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "primer JB586"
US-08-968-505-15

  Query Match            75.8%;  Score 14.4;  DB 3;  Length 20;
  Best Local Similarity  93.8%;  Pred. No. 76;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 GGCCATCAGTGCTCTG 19
           ||| ||||||||||||
Db       2 GGCAATCAGTGCTCTG 17


RESULT 7
US-09-233-506-11/c
; Sequence 11, Application US/09233506
; Patent No. 6136580
; GENERAL INFORMATION:
;  APPLICANT: Fukuda, Minoru
;  APPLICANT: Yeh, Jiunn-Chern
;  TITLE OF INVENTION: A Beta-1-6-N-Acetylglucosaminytransferase That Forms
;  TITLE OF INVENTION: Core 2, Core 4 and I Branches
;  FILE REFERENCE: P-LJ 3415
;  CURRENT APPLICATION NUMBER: US/09/233,506
;  CURRENT FILING DATE: 1999-01-19
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 33
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-233-506-11

  Query Match            69.5%;  Score 13.2;  DB 3;  Length 33;
  Best Local Similarity  83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCT 18
           |||| |||||  ||||||
Db      24 CTGGACCATCTCTGCTCT 7


RESULT 8
US-08-584-040-4815/c
; Sequence 4815, Application US/08584040
; Patent No. 6346398
```

```
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  4815:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      OTHER INFORMATION:  The letter "N" represents the stem II region
;      OTHER INFORMATION:  of an HH ribozyme.
US-08-584-040-4815

  Query Match             68.4%;  Score 13;  DB 4;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CATCAGTGCTCTG 19
              |||||||||||||
Db         14 CATCAGTGCTCTG 2


RESULT 9
US-09-182-728A-4/c
; Sequence 4, Application US/09182728A
; Patent No. 6238883
; GENERAL INFORMATION:
;  APPLICANT:  BROWN, ANTHONY
;  APPLICANT:  CHAPMAN, CONRAD GERALD
;  APPLICANT:  GLOGER, ISRAEL SIMON
;  APPLICANT:  EVANS, JOANNE RACHEL
;  APPLICANT:  CAIRNS, WILLIAM
;  APPLICANT:  HERDON, HUGH
;  TITLE OF INVENTION:  NOVEL COMPOUNDS
;  FILE REFERENCE:  GP-30176
;  CURRENT APPLICATION NUMBER: US/09/182,728A
;  CURRENT FILING DATE:  1998-10-29
;  PRIOR APPLICATION NUMBER:  9818890.7
;  PRIOR FILING DATE:  1998-08-28
;  NUMBER OF SEQ ID NOS:  6
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-09-182-728A-4

  Query Match             67.4%;  Score 12.8;  DB 4;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTGGGCCATCAGTGCT 16
              ||||||  ||||||||
Db         21 CTGGGCACTCAGTGCT 6


RESULT 10
US-09-795-232-4/c
; Sequence 4, Application US/09795232
; Patent No. 6426405
; GENERAL INFORMATION:
;  APPLICANT:  Anthony M. Brown
;  APPLICANT:  Conrad Gerald Chapman
;  APPLICANT:  Israel Simon Gloger
;  APPLICANT:  Joanne Rachel Evans
;  APPLICANT:  William Cairns
;  APPLICANT:  Hugh Jonathan Herdon
;  TITLE OF INVENTION:  NOVEL COMPOUNDS
;  FILE REFERENCE:  GP-30176-D1
;  CURRENT APPLICATION NUMBER: US/09/795,232
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER:  09/182,728
;  PRIOR FILING DATE:  1998-10-29
;  PRIOR APPLICATION NUMBER:  9818890.7
;  PRIOR FILING DATE:  1998-08-28
;  NUMBER OF SEQ ID NOS:  6
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-09-795-232-4

  Query Match             67.4%;  Score 12.8;  DB 4;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTGGGCCATCAGTGCT 16
              ||||||  ||||||||
Db         21 CTGGGCACTCAGTGCT 6


RESULT 11
US-08-960-190A-2
; Sequence 2, Application US/08960190A
; Patent No. 6232445
;  GENERAL INFORMATION:
;    APPLICANT:  Rhode, Peter R.
;    APPLICANT:  Acevedo, Jorge
;    APPLICANT:  Burkhardt, Martin
;    APPLICANT:  Jiao, Jin-an
;    APPLICANT:  Wong, Hing C.
;    TITLE OF INVENTION:  SOLUBLE MHC COMPLEXES AND
;    TITLE OF INVENTION:  METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dike, Bronstein, Roberts & Cushman, LLP
;      STREET:  130 Water Street
```

```
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  usa
;       ZIP:  02109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/960,190A
;       FILING DATE:  29-OCT-1997
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Corless, Peter F
;       REGISTRATION NUMBER:  33,860
;       REFERENCE/DOCKET NUMBER:  48002
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-523-3400
;       TELEFAX:  617-523-6440
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  43 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-960-190A-2

  Query Match             66.3%;  Score 12.6;  DB 4;  Length 43;
  Best Local Similarity   78.9%;  Pred. No. 7.1e+02;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCTG 19
           | |||||| ||  ||||||
Db      13 CCGGGCCACCATGGCTCTG 31


RESULT 12
US-08-596-387B-40
; Sequence 40, Application US/08596387B
; Patent No. 5869270
;  GENERAL INFORMATION:
;    APPLICANT:  Rhode, Peter R.
;    APPLICANT:  Jiao, Jin-An
;    APPLICANT:  Burkhardt, Martin
;    APPLICANT:  Wong, Hing
;    TITLE OF INVENTION:  MHC COMPLEXES AND USES THEREOF
;    NUMBER OF SEQUENCES:  124
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dade International, Inc.
;      STREET:  1717 Deerfield Road
;      CITY:  Deerfield
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60015
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/596,387B
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/09816
;      FILING DATE:  31-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/382,454
;      FILING DATE:  01-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/283,302
;      FILING DATE:  29-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pearson, Louise S.
;      REGISTRATION NUMBER:  32,369
;      REFERENCE/DOCKET NUMBER:  STR-4665-CIP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (708) 267-5300
;      TELEFAX:  (708) 267-5376
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  44 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
US-08-596-387B-40

  Query Match             66.3%;  Score 12.6;  DB 2;  Length 44;
  Best Local Similarity   78.9%;  Pred. No. 7.1e+02;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCTG 19
           | |||||| ||  ||||||
Db      14 CCGGGCCACCATGGCTCTG 32


RESULT 13
US-09-067-615-40
; Sequence 40, Application US/09067615
; Patent No. 6309645
;  GENERAL INFORMATION:
;    APPLICANT:  Rhode, Peter R.
;    APPLICANT:  Jiao, Jin-An
;    APPLICANT:  Burkhardt, Martin
;    APPLICANT:  Wong, Hing
;    TITLE OF INVENTION:  MHC COMPLEXES AND USES THEREOF
;    NUMBER OF SEQUENCES:  124
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dade International, Inc.
;      STREET:  1717 Deerfield Road
;      CITY:  Deerfield
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60015
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/067,615
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/596,387
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/382,454
;      FILING DATE:  01-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/283,302
;      FILING DATE:  29-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pearson, Louise S.
;      REGISTRATION NUMBER:  32,369
;      REFERENCE/DOCKET NUMBER:  STR-4665-CIP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (708) 267-5300
;      TELEFAX:  (708) 267-5376
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
```

```
;       LENGTH:  44 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  unknown
;       TOPOLOGY:  unknown
US-09-067-615-40

  Query Match             66.3%;  Score 12.6;  DB 4;  Length 44;
  Best Local Similarity   78.9%;  Pred. No. 7.1e+02;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCTG 19
           | ||||||  ||  ||||||
Db      14 CCGGGCCACCATGGCTCTG 32


RESULT 14
PCT-US95-09816A-40
; Sequence 40, Application PC/TUS9509816A
;  GENERAL INFORMATION:
;    APPLICANT:  Wong, Hing C.
;    APPLICANT:  Rhode, Peter R.
;    APPLICANT:  Widanz, Jon A.
;    APPLICANT:  Grammer, Susan
;    APPLICANT:  Edwards, Ana C.
;    APPLICANT:  Chavaillaz, Pierre-Andre
;    APPLICANT:  Jiao, Jin-An
;    TITLE OF INVENTION:  MHC COMPLEXES AND USES THEREOF
;    NUMBER OF SEQUENCES:  123
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dade International, Inc.
;      STREET:  1717 Deerfield Road
;      CITY:  Deerfield
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60015
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/09816A
;      FILING DATE:  31-JUL-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/382,454
;      FILING DATE:  01-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/283,302
;      FILING DATE:  29-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pearson, Louise S.
;      REGISTRATION NUMBER:  32,369
;      REFERENCE/DOCKET NUMBER:  STR-4665-CIP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (708) 267-5300
;      TELEFAX:  (708) 267-5376
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  44 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
PCT-US95-09816A-40

  Query Match             66.3%;  Score 12.6;  DB 5;  Length 44;
  Best Local Similarity   78.9%;  Pred. No. 7.1e+02;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCTG 19
           | ||||||  ||  ||||||
Db      14 CCGGGCCACCATGGCTCTG 32


RESULT 15
US-08-773-731A-12/c
; Sequence 12, Application US/08773731A
; Patent No. 6100056
;  GENERAL INFORMATION:
;    APPLICANT:  Gasson, Michael J.
;    APPLICANT:  Dodd, Helen M.
;    TITLE OF INVENTION:  NISINS
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DICKSTEIN, SHAPIRO, MORIN & OSHINSKY LLP
;      STREET:  2101 L Street N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/773,731A
;      FILING DATE:  24-DEC-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/313,123
;      FILING DATE:  18-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB93/00676
;      FILING DATE:  01-APR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9207267.7
;      FILING DATE:  02-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brady, Jr., James W.
;      REGISTRATION NUMBER:  32,115
;      REFERENCE/DOCKET NUMBER:  E8280.016/P016
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-785-9700
;      TELEFAX:  202-887-0689
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "primer"
US-08-773-731A-12

  Query Match             65.3%;  Score 12.4;  DB 3;  Length 18;
  Best Local Similarity   92.9%;  Pred. No. 8e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       6 CCATCAGTGCTCTG 19
           ||||||| ||||||
Db      14 CCATCAGAGCTCTG 1


Search completed: November 28, 2002, 19:32:51
Job time : 39.3276 secs
```

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 15:32:44 ; Search time 176.241 Seconds
(without alignments)
242.780 Million cell updates/sec

Title: US-09-719-737-18
Perfect score: 19
Sequence: 1 ctgggccatcagtgctctg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	19	100.0	19	21	AAZ57602	Antisense oligonuc
c	2	15.8	83.2	45	16	AAQ95044	Human hippocampal
	3	14.8	77.9	45	16	AAQ95043	Human hippocampal
	4	14.4	75.8	20	19	AAV43277	Primer JB586 for a
	5	14.2	74.7	20	20	AAX97497	Primer used to amp
c	6	14.2	74.7	36	22	AAH41073	PCR primer specifi
c	7	13.4	70.5	47	21	AAZ66407	Human map-related
c	8	13.2	69.5	33	22	AAC62140	PCR primer for bet
	9	13.2	69.5	47	21	AAZ66460	Human map-related
c	10	13	68.4	25	22	AAH38907	SNP specific SNPE
c	11	13	68.4	27	18	AAX72065	Mouse flk-1 VEGF r
c	12	13	68.4	27	21	AAZ62041	Hammerhead ribozym
c	13	13	68.4	29	21	AAF06658	Hammerhead ribozym
c	14	13	68.4	29	21	AAA24583	Oestrogen receptor
c	15	12.8	67.4	17	24	ABN06590	Human GDMLP-1 17-m
c	16	12.8	67.4	17	24	ABN06591	Human GDMLP-1 17-m
c	17	12.8	67.4	25	21	AAZ95538	Human SC polypepti
c	18	12.8	67.4	25	24	ABN11482	Human GDMLP-1 25-m
c	19	12.8	67.4	25	24	ABN11483	Human GDMLP-1 25-m
c	20	12.8	67.4	25	24	ABN11484	Human GDMLP-1 25-m
c	21	12.8	67.4	25	24	ABN11485	Human GDMLP-1 25-m
c	22	12.8	67.4	25	24	ABN11486	Human GDMLP-1 25-m
c	23	12.8	67.4	25	24	ABN11487	Human GDMLP-1 25-m
c	24	12.8	67.4	25	24	ABN11488	Human GDMLP-1 25-m
c	25	12.8	67.4	25	24	ABN11489	Human GDMLP-1 25-m
c	26	12.8	67.4	25	24	ABN11490	Human GDMLP-1 25-m
c	27	12.8	67.4	25	24	ABN11491	Human GDMLP-1 25-m
	28	12.8	67.4	39	21	AAZ96575	T cell antigen rec
c	29	12.8	67.4	50	22	AAL31163	Human SNP oligonuc
	30	12.6	66.3	19	22	AAH37830	SNP specific lower
	31	12.6	66.3	30	22	AAF75322	Extended TOGA prim
	32	12.6	66.3	43	20	AAX89047	PCR primer OPR132
	33	12.6	66.3	44	17	AAT34718	PCR primer OPR132
	34	12.6	66.3	44	18	AAT86972	Primer used in MHC
	35	12.6	66.3	47	21	AAZ67507	Human map-related
	36	12.6	66.3	48	19	AAV22976	PCR primer tau-dl-
	37	12.6	66.3	48	20	AAV70655	PCR primer tau-dl-
	38	12.6	66.3	50	22	AAL27963	Human SNP oligonuc
c	39	12.6	66.3	50	22	AAL33541	Human SNP oligonuc
	40	12.6	66.3	50	23	ABL00017	Human silent nonco
	41	12.4	65.3	17	24	ABN97702	Human NEDD-1 scann
	42	12.4	65.3	17	24	ABN97703	Human NEDD-1 scann
	43	12.4	65.3	17	24	ABN97704	Human NEDD-1 scann
	44	12.4	65.3	17	24	ABN97705	Human NEDD-1 scann
c	45	12.4	65.3	18	14	AAQ50297	PCR primer for pre

ALIGNMENTS

RESULT 1
AAZ57602
ID AAZ57602 standard; DNA; 19 BP.
XX
AC AAZ57602;
XX
DT 28-MAR-2000 (first entry)
XX
DE Antisense oligonucleotide CCR3AS to inhibit CCR3 receptor expression.
XX
KW Antisense oligonucleotide; CCR3 receptor; chemokine receptor; asthma;
KW allergy; cancer; receptor expression inhibitor; hypereosinophilia;
KW inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO9966037-A2.
XX
PD 23-DEC-1999.
XX
PF 17-JUN-1999; 99WO-CA00572.
XX
PR 17-JUN-1998; 98CA-2235420.
XX
PA (REEX-) RECH EXPERTISES & DEV MEDICAUX PARENZ IN.
XX
PI Renzi P;
XX
DR WPI; 2000-097743/08.
XX
PT Antisense oligonucleotides directed to CCR3, interleukin or granulocyte
PT macrophage colony stimulating factor receptors, used for treating or

```
PT   preventing asthma, allergies, hypereosinophilia, inflammation or cancer
PT   .
XX
PS   Claim 5; Page 32; 72pp; English.
XX
CC   This is an antisense oligonucleotide directed against the CCR3 receptor.
CC   The antisense oligonucleotide inhibits CCR3 receptor expression. The CCR3
CC   receptor is important in the recruitment of eosinophils into the sites of
CC   allergic or asthmatic inflammation. The chemokines Eotaxin, MCP-4 and
CC   RANTES mediate most of their effects through the CCR3 receptor. The
CC   invention relates to antisense oligonucleotides directed against a
CC   nucleic acid sequence encoding either a CCR3 receptor, a common subunit
CC   of interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common
CC   subunit of IL-3, IL-5 and GM-CSF receptors. The antisense
CC   oligonucleotides can be used in the treatment or prevention of asthma,
CC   allergy, hypereosinophilia, general inflammation or cancer.
XX
SQ   Sequence 19 BP; 2 A; 6 C; 6 G; 5 T; 0 other;

  Query Match           100.0%;  Score 19;  DB 21;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 2.7;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCTG 19
           |||||||||||||||||||
Db       1 CTGGGCCATCAGTGCTCTG 19


RESULT 2
AAQ95044/c
ID   AAQ95044 standard; DNA; 45 BP.
XX
AC   AAQ95044;
XX
DT   06-MAR-1996  (first entry)
XX
DE   Human hippocampal neuropeptide Y2 receptor (-) strand DNA probe TM4.
XX
KW   Hippocampus; brain; neuropeptide; peptide; hypertension; pain;
KW   gastrointestinal disorder; diagnosis; sleeping disorder; epilepsy;
KW   memory loss; diarrhorea; nasal congestion; DNA probe;
KW   oligonucleotide; ss.
XX
OS   Synthetic.
XX
PN   WO9521245-A1.
XX
PD   10-AUG-1995.
XX
PF   03-FEB-1995;   95WO-US01469.
XX
PR   03-FEB-1994;   94US-0192288.
XX
PA   (SYNA-) SYNAPTIC PHARM CORP.
XX
PI   Branchek T,  Gerald C,  Walker MW,  Weinshank R;
XX
DR   WPI; 1995-283765/37.
XX
PT   Human and rat Y2 receptor DNA and protein - useful in diagnosis and
PT   treatment of e.g. cognitive and gastrointestinal disorder(s),
PT   hypertension and pain
XX
PS   Disclosure; Page 50; 193pp; English.
XX
CC   This oligonucleotide probe corresponding to nucleotides 531-600 of
CC   human neuropeptide Y2 receptor cDNA and to a transmembrane region
CC   of the amino acid sequence of the receptor, was used to obtain the
CC   rat homologue of the human Y2 receptor.
XX
SQ   Sequence 45 BP; 10 A; 13 C; 17 G; 5 T; 0 other;

  Query Match           83.2%;  Score 15.8;  DB 16;  Length 45;
  Best Local Similarity  89.5%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCTG 19
           ||||| |||||||||| |||
Db      43 CTGGGGCATCAGTGCCCTG 25


RESULT 3
AAQ95043
ID   AAQ95043 standard; DNA; 45 BP.
XX
AC   AAQ95043;
XX
DT   06-MAR-1996  (first entry)
XX
DE   Human hippocampal neuropeptide Y2 receptor (+) strand DNA probe TM4.
XX
KW   Hippocampus; brain; neuropeptide; peptide; hypertension; pain;
KW   gastrointestinal disorder; diagnosis; sleeping disorder; epilepsy;
KW   memory loss; diarrhorea; nasal congestion; DNA probe;
KW   oligonucleotide; ss.
XX
OS   Synthetic.
XX
PN   WO9521245-A1.
XX
PD   10-AUG-1995.
XX
PF   03-FEB-1995;   95WO-US01469.
XX
PR   03-FEB-1994;   94US-0192288.
XX
PA   (SYNA-) SYNAPTIC PHARM CORP.
XX
PI   Branchek T,  Gerald C,  Walker MW,  Weinshank R;
XX
DR   WPI; 1995-283765/37.
XX
PT   Human and rat Y2 receptor DNA and protein - useful in diagnosis and
PT   treatment of e.g. cognitive and gastrointestinal disorder(s),
PT   hypertension and pain
XX
PS   Disclosure; Page 50; 193pp; English.
XX
CC   This oligonucleotide probe corresponding to nucleotides 531-600 of
CC   human neuropeptide Y2 receptor cDNA and to a transmembrane region
CC   of the amino acid sequence of the receptor, was used to obtain the
CC   rat homologue of the human Y2 receptor.
XX
SQ   Sequence 45 BP; 7 A; 12 C; 12 G; 14 T; 0 other;

  Query Match           77.9%;  Score 14.8;  DB 16;  Length 45;
  Best Local Similarity  88.9%;  Pred. No. 4.2e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCT 18
           ||||| |||||||||  ||
Db      28 CTGGGGCATCAGTGCCCT 45


RESULT 4
AAV43277
ID   AAV43277 standard; DNA; 20 BP.
XX
AC   AAV43277;
XX
DT   26-OCT-1998  (first entry)
XX
DE   Primer JB586 for amplication-based detection of fungal ITS regions.
XX
KW   Internal transcribed spacer; ITS; detection; maize; fungal pathogen;
KW   PCR primer; ss.
```

XX
OS Synthetic.
OS Helminthosporium turcicum.
XX
PN EP859061-A2.
XX
PD 19-AUG-1998.
XX
PF 03-NOV-1997; 97EP-0810779.
XX
PR 01-NOV-1996; 96US-0742023.
XX
PA (NOVS) NOVARTIS AG.
XX
PI Beck JJ;
XX
DR WPI; 1998-429687/37.
XX
PT New internal transcribed spacer sequences of maize fungal pathogens
PT and primers and primer pairs - used to detect pathogens e.g.
PT Helminthosporium carbonum, Cercospora zeae-maydis and Kabatiella
PT zeae
XX
PS Claim 4; Page 11; 49pp; English.
XX
CC PCR primers AAV43277-303 are used to in amplification-based detction of
CC maize fungal internal transcribed spacer (ITS) regions. They are used
CC to identify Helminthosporium turcicum, H. maydis, H. carbonum,
CC Kabatiella zeae and Cercospora zeae-maydis. The method comprises
CC isolating DNA from a plant leaf infected with a pathogen, subjecting the
CC DNA to PCR amplification using at least one primer derived from the ITS
CC sequence.
XX
SQ Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 other;

Query Match 75.8%; Score 14.4; DB 19; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GGCCATCAGTGCTCTG 19
||| ||||||||||||
Db 2 GGCAATCAGTGCTCTG 17

RESULT 5
AAX97497
ID AAX97497 standard; DNA; 20 BP.
XX
AC AAX97497;
XX
DT 13-SEP-1999 (first entry)
XX
DE Primer used to amplify Chlamydia pneumoniae polynucleotides.
XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope; PCR primer; ss.
XX
OS Synthetic.
OS Chlamydia pneumoniae.
XX
PN WO9927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98WO-IB01890.
XX
PR 04-NOV-1998; 98US-0107078.
PR 21-NOV-1997; 97FR-0014673.
XX
PA (GEST) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-357842/30.
XX
PT Genome sequence of Chlamydia pneumoniae
XX
PS Page 1909; Disclosure; 1912pp; English.
XX
CC AAX91991-X97517 represent PCR primers used to amplify open reading
CC frames and other nucleic acid sequences from the genome of
CC Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory
CC disease such as pneumonia and bronchitis and is thought to be a
CC contributing factor in heart disease, sarcoidosis, sinusitis, purulent
CC otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
CC by the open reading frames of the C. pneumoniae genome (see AAY34584-
CC AAY35879) can be used in immunogenic compositions as vaccines. Vectors
CC containing C. pneumoniae nucleotides sequences can also be used as
CC immunogenic compositions, especially where the vector directs the
CC expression of a neutralising epitope of C. pneumoniae.
XX
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 other;

Query Match 74.7%; Score 14.2; DB 20; Length 20;
Best Local Similarity 84.2%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGGGCCATCAGTGCTCTG 19
|||| |||| ||| |||||
Db 1 CTGGACCATAAGTACTCTG 19

RESULT 6
AAH41073/c
ID AAH41073 standard; DNA; 36 BP.
XX
AC AAH41073;
XX
DT 03-SEP-2001 (first entry)
XX
DE PCR primer specific for ecydsone C-terminus insertion site DNA SEQ ID 29.
XX
KW Steroid hormone; thyroid hormone; receptor; DNA binding; PCR primer;
KW chimeric protein; expression modulation; ecdysone receptor; ss.
XX
OS Unidentified.
XX
PN WO200136447-A2.
XX
PD 25-MAY-2001.
XX
PF 17-OCT-2000; 2000WO-US41224.
XX
PR 20-OCT-1999; 99US-0421971.
XX
PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Gage FH, Suhr ST, Gil EB, Senut MC;
XX
DR WPI; 2001-355608/37.
XX
PT Novel chimeric protein useful for modulating exogenous gene expression
PT in subjects, comprises two functional protein units, each containing
PT dimerization domain of steroid/thyroid hormone nuclear receptor
PT superfamily -
XX
PS Example 1; Page 39; 60pp; English.
XX
CC The present invention relates to a chimeric protein which consists of at
CC least two functional protein units where each protein unit comprises the
CC dimerisation domain of a member of the steroid/thyroid hormone nuclear
CC receptor superfamily. The protein units are linked by a linker peptide,
CC and the two protein units form a functional entity. The invention
CC includes a method for modulating the expression of an exogenous gene in
CC an organism or cell containing the chimeric protein. The cell or organism

```
CC   also contains a DNA construct comprising the exogenous gene under the
CC   control of a response element with which the chimeric protein interacts.
CC   The response element controls the expression of the exogenous gene. The
CC   method also involves administering to the subject or cell an effective
CC   amount of an exogenous ligand for at least one functional unit of the
CC   chimeric protein. The chimeric protein is useful for modulating the
CC   expression of an exogenous gene in a subject organism. The present
CC   sequence represents a PCR primer specific for DNA encoding the C-terminus
CC   insertion site of the ecdysone receptor. The PCR product is used in an
CC   example illustrating the construction of a chimeric protein of the
CC   invention.
XX
SQ   Sequence 36 BP; 6 A; 9 C; 12 G; 9 T; 0 other;

  Query Match             74.7%;  Score 14.2;  DB 22;  Length 36;
  Best Local Similarity   84.2%;  Pred. No. 8.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCTG 19
           |||||||| ||| || |||
Db      27 CTGGGCCAACAGGGCCCTG 9


RESULT 7
AAZ66407/c
ID   AAZ66407 standard; DNA; 47 BP.
XX
AC   AAZ66407;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human map-related biallelic marker SEQ ID NO:754.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(24,G)
FT                   /*tag= a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB00822.
XX
PR   21-APR-1998;   98US-0082614.
PR   23-NOV-1998;   98US-0109732.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome -
XX
PS   Claim 1; Page 391; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the
CC   invention have a variety of uses: they can be used for high density
CC   mapping of the human genome, and in complex association studies and
CC   haplotyping studies which are useful in determining the genetic basis
CC   for disease states. Compositions and methods of the invention can also
CC   be useful for the identification of the targets for the development of
CC   pharmaceutical agents and diagnostic methods, as well as the
CC   characterisation of the differential efficacious responses to and side
CC   effects from pharmaceutical agents acting on a disease as well as other
CC   treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC   and 3367, are not actually given a sequence in the Sequence Listing
CC   from the present invention.
XX
SQ   Sequence 47 BP; 12 A; 17 C; 8 G; 10 T; 0 other;

  Query Match             70.5%;  Score 13.4;  DB 21;  Length 47;
  Best Local Similarity   93.3%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 GGGCCATCAGTGCTC 17
           ||| ||||||||||
Db      34 GGGGCATCAGTGCTC 20


RESULT 8
AAC62140/c
ID   AAC62140 standard; DNA; 33 BP.
XX
AC   AAC62140;
XX
DT   06-MAR-2001  (first entry)
XX
DE   PCR primer for beta-1-6-N-acetylglucosaminyltransferase DNA fragment.
XX
KW   Human; beta-1-6-N-acetylglucosaminyltransferase; C2GnT-M; inflammation;
KW   membrane protein; branched sialyl Lex; L-selectin; immune reaction;
KW   inflammation; tissue rejection; tumour metastasis; PCR primer; ss.
XX
OS   Mus musculus.
XX
PN   US6136580-A.
XX
PD   24-OCT-2000.
XX
PF   19-JAN-1999;   99US-0233506.
XX
PR   19-JAN-1999;   99US-0233506.
XX
PA   (BURN-) BURNHAM INST.
XX
PI   Fukuda M,  Yeh J;
XX
DR   WPI; 2001-040238/05.
XX
PT   New C2GnT-M polypeptides having core 2, core 4 and I branching
PT   beta-1-6-N-acetylglucosaminyltransferase activities for preparing
PT   reagents useful for diagnosing, preventing or treating inflammation or
PT   tumour metastasis -
XX
PS   Example 5; Column 21; 25pp; English.
XX
CC   PCR primers AAC62140-41 were used to amplify a DNA fragment encoding a
CC   beta-1-6-N-acetylglucosaminyltransferase polypeptide, with core2, core4
CC   and I branching activities. It is designated C2GnT-M. C2GnT-M is a
CC   membrane protein that is predominantly expressed in colon, small
CC   intestine, trachea, stomach and thyroid, as well as in certain cancer
CC   cell lines. C2GnT-M polypeptides may be used to prepare molecules having
CC   highly branched sialyl Lex and L-selectins, which may be subsequently
CC   used to modulate immune reactions, e.g. inflammation and tissue
CC   rejection, and to prevent or inhibit tumour metastasis.
XX
SQ   Sequence 33 BP; 8 A; 8 C; 10 G; 7 T; 0 other;

  Query Match             69.5%;  Score 13.2;  DB 22;  Length 33;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy       1 CTGGGCCATCAGTGCTCT 18
           |||| |||||  ||||||
Db      24 CTGGACCATCTCTGCTCT 7
```

```
RESULT 9
AAZ66460
ID   AAZ66460 standard; DNA; 47 BP.
XX
AC   AAZ66460;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human map-related biallelic marker SEQ ID NO:807.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(24,C)
FT                   /*tag= a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB00822.
XX
PR   21-APR-1998;   98US-0082614.
PR   23-NOV-1998;   98US-0109732.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome  -
XX
PS   Claim 1; Page 402; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the
CC   invention have a variety of uses: they can be used for high density
CC   mapping of the human genome, and in complex association studies and
CC   haplotyping studies which are useful in determining the genetic basis
CC   for disease states. Compositions and methods of the invention can also
CC   be useful for the identification of the targets for the development of
CC   pharmaceutical agents and diagnostic methods, as well as the
CC   characterisation of the differential efficacious responses to and side
CC   effects from pharmaceutical agents acting on a disease as well as other
CC   treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC   and 3367, are not actually given a sequence in the Sequence Listing
CC   from the present invention.
XX
SQ   Sequence 47 BP; 10 A; 12 C; 15 G; 10 T; 0 other;
```

```
  Query Match             69.5%;  Score 13.2;  DB 21;  Length 47;
  Best Local Similarity   83.3%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 TGGGCCATCAGTGCTCTG 19
           |||||| | || ||||||
Db      15 TGGGCCTTGAGAGCTCTG 32
```

```
RESULT 10
AAH38907/c
ID   AAH38907 standard; DNA; 25 BP.
XX
AC   AAH38907;
XX
DT   14-AUG-2001  (first entry)
XX
DE   SNP specific SNPE primer SEQ ID 1703.
XX
KW   Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW   SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW   Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW   polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW   acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW   inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200129262-A2.
XX
PD   26-APR-2001.
XX
PF   13-OCT-2000; 2000WO-US28436.
XX
PR   15-OCT-1999;   99US-0160096.
XX
PA   (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI   Picoult-Newburg L,  Pohl M;
XX
DR   WPI; 2001-290930/30.
XX
PT   New genotyping oligonucleotide, useful for detecting the presence,
PT   absence or identity of single polynucleotide polymorphism in a nucleic
PT   acid sample  -
XX
PS   Claim 1; Page 58; 83pp; English.
XX
CC   Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC   primer extension (SNPE) primers, and the sequences of regions flanking
CC   sites of single nucleotide polymorphisms SNPs. The present invention
CC   includes kits for determining the presence or absence of a SNP, using the
CC   oligonucleotides of the invention. The PCR primers are used to amplify a
CC   SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC   The oligonucleotides are useful for genotyping a nucleic acid sample by
CC   performing a single-nucleotide primer extension reaction. The
CC   oligonucleotides are useful for determining the presence, absence or
CC   identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC   assess by association analysis the genotype of an individual or group of
CC   individuals, having a pathological phenotypic trait suspected of being
CC   caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC   agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC   dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC   osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC   traits also include symptoms of or susceptibility to multifactorial
CC   disease of which a component is or may be genetic such as autoimmune
CC   diseases, including, rheumatoid arthritis, multiple sclerosis,
CC   inflammation, cancer, nervous system diseases and infection by pathogenic
CC   microorganism. The method is also useful in forensic investigations and
CC   paternity analysis. The present sequence represents a single nucleotide
CC   primer extension (SNPE) primer specific for a human SNP containing DNA
CC   sequence.
XX
SQ   Sequence 25 BP; 4 A; 4 C; 10 G; 6 T; 1 other;
```

```
  Query Match             68.4%;  Score 13;  DB 22;  Length 25;
  Best Local Similarity   86.7%;  Pred. No. 3.2e+03;
  Matches   13;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 GCCATCAGTGCTCTG 19
```

```
          |||:|||| ||||||
Db      19 GCCRTCAGAGCTCTG 5


RESULT 11
AAX72065/c
ID   AAX72065 standard; RNA; 27 BP.
XX
AC   AAX72065;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Mouse flk-1 VEGF receptor hammerhead ribozyme #309.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW   flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Synthetic.
OS   Mus sp.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US17480.
XX
PR   11-JAN-1996;   96US-0584040.
PR   26-OCT-1995;   95US-0005974.
XX
PA   (CHIR ) CHIRON CORP.
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Escobedo J,  McSwiggen J,  Pavco P,  Stinchcomb D;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT   mRNA stability  - useful for treating e.g. tumour angiogenesis,
PT   psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS   Claim 9; Page 132; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC   be treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention.
XX
SQ   Sequence 27 BP; 10 A; 5 C; 7 G; 4 U; 1 other;

  Query Match             68.4%;  Score 13;  DB 18;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 CATCAGTGCTCTG 19
           |||||||||||||
Db      14 CATCAGTGCTCTG 2


RESULT 12
AAZ62041/c
ID   AAZ62041 standard; RNA; 27 BP.
XX
AC   AAZ62041;
XX
DT   28-MAR-2000  (first entry)
XX
DE   Hammerhead ribozyme HCV-2704 cleaves HCV RNA at nt. Position 2704.
XX
KW   Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW   cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW   autoimmune disease; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 16
FT                   /*tag=  a
FT                   /note= "hammerhead ribozyme stem-loop II (as defined
FT                          by Hertel et al., NAR 20:3252 (1992))"
XX
PN   WO9955847-A2.
XX
PD   04-NOV-1999.
XX
PF   26-APR-1999;   99WO-US09027.
XX
PR   27-APR-1998;   98US-0083217.
PR   18-SEP-1998;   98US-0100842.
PR   25-FEB-1999;   99US-0257608.
PR   23-MAR-1999;   99US-0274553.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  McSwiggen JA,  Roberts E,  Pavco PA,  Macejak D;
XX
DR   WPI; 2000-062023/05.
XX
PT   Novel ribozymes for the treatment of diseases and conditions related to
PT   hepatitis C infection  -
XX
PS   Claim 8; Page 55; 123pp; English.
XX
CC   The present sequence represents an enzymatic nucleic acid, especially
CC   a hammerhead ribozyme, which cleaves the Hepatitis C virus (HCV) RNA
CC   sequence at the base position indicated in the descriptor line.
CC   The HCV sequence was screened for optimal ribozyme target sites using
CC   a computer folding algorithm and regions of the mRNA which did not form
CC   secondary folding structures and contained potential ribozyme cleavage
CC   sites were identified.  Ribozymes were synthesised to target these sites
CC   and their activities optimised by either varying the length of the
CC   binding arms or by modification to prevent degradation by nucleases.
CC   The ribozymes of the invention inhibit gene expression and/or viral
CC   replication, and are used to treat diseases associated with Hepatitis C
CC   virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular
CC   carcinoma. The ribozymes may be used in combination with interferon to
CC   treat HCV infection, other infectious diseases, autoimmune diseases, and
CC   cancer.
XX
SQ   Sequence 27 BP; 8 A; 7 C; 8 G; 3 U; 1 other;

  Query Match             68.4%;  Score 13;  DB 21;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 CATCAGTGCTCTG 19
           |||||||||||||
Db      13 CATCAGTGCTCTG 1


RESULT 13
AAF06658/c
ID   AAF06658 standard; RNA; 29 BP.
XX
AC   AAF06658;
XX
DT   16-FEB-2001  (first entry)
XX
```

DE Hammerhead ribozyme #3455.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US09721.
XX
PR 12-APR-1999; 99US-0129390.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor
PT protein, interferon alpha and erythropoietin -
XX
PS Claim 59; Page 135; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
CC transcription factor gene, IRF-2 and/or the CAATT Displacement
CC Protein (CDP). Inhibition of the repressors removes prevents
CC inhibition (and consequently increases expression of) genes involved in
CC the production of erythropoietin, granulocyte colony stimulating factor
CC protein and interferon alpha.
XX
SQ Sequence 29 BP; 9 A; 7 C; 10 G; 2 U; 1 other;

Query Match 68.4%; Score 13; DB 21; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CATCAGTGCTCTG 19
||||||||||||||
Db 14 CATCAGTGCTCTG 2

RESULT 14
AAA24583/c
ID AAA24583 standard; RNA; 29 BP.
XX
AC AAA24583;
XX
DT 19-JUL-2000 (first entry)
XX
DE Oestrogen receptor hammerhead ribozyme sequence SEQ ID NO:1081.
XX
KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9954459-A2.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-US08547.
XX
PR 20-APR-1998; 98US-0082404.
PR 23-JUN-1998; 98US-0103636.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;
PI Matulic-Adamic J;
XX
DR WPI; 2000-013248/01.
XX
PT New nucleic acids that interact, and optionally cleave, target
PT sequences, used to treat cancer -
XX
PS Claim 51; Page 91; 148pp; English.
XX
CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphoro(di)thioate
CC link, having endonuclease activity. (A), and more generally any
CC catalytic nucleic acid (A') that modulates expression of the oestrogen
CC receptor gene, are used to treat cancer (particularly of breast or
CC endometrium), in vivo or by transforming cells ex vivo and implanting
CC treated cells, or for other conditions associated with levels of
CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
CC can also be used to correlate inhibition of gene expression with
CC alterations in phenotype, particularly for identification of therapeutic
CC targets, and as research reagents (for RNA, in the same way that
CC restriction endonucleases are used with DNA). The combination of
CC modifications in (A) improves resistance to nucleases, binding affinity
CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
CC their corresponding target sequences. AAA26219 to AAA26271 represent
CC other ribozyme sequences and antisense oligonucleotides used in the
CC exemplification of the present invention.
XX
SQ Sequence 29 BP; 12 A; 5 C; 7 G; 4 U; 1 other;

Query Match 68.4%; Score 13; DB 21; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CATCAGTGCTCTG 19
||||||||||||||
Db 14 CATCAGTGCTCTG 2

RESULT 15
ABN06590/c
ID ABN06590 standard; DNA; 17 BP.
XX
AC ABN06590;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6582.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US16981.
XX
PR 26-MAY-2000; 2000US-207456P.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.

PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 05-FEB-2001; 2001US-266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption ionization, comprises human
PT myosin-like protein hGDMLP-1 -
XX
PS Disclosure; SEQ ID 6582; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
CC hGDMLP-1 can be used in gene therapy and vaccine production. The
CC hGDMLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMLP-1, in
CC particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX
SQ Sequence 17 BP; 4 A; 5 C; 6 G; 2 T; 0 other;

Query Match 67.4%; Score 12.8; DB 24; Length 17;
Best Local Similarity 87.5%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       1 CTGGGCCATCAGTGCT 16
           |||| || ||||||||
Db      17 CTGGACCCTCAGTGCT 2
```

Search completed: November 28, 2002, 17:24:12
Job time : 176.575 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 28, 2002, 16:42:34 ; Search time 1103.97 Seconds
(without alignments)
500.879 Million cell updates/sec

Title: US-09-719-737-18
Perfect score: 19
Sequence: 1 ctgggccatcagtgctctg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		19	100.0	19	6	AX008665	AX008665 Sequence
c 2		19	100.0	19	6	AX008666	AX008666 Sequence
c 3		15.8	83.2	45	6	AR088050	AR088050 Sequence
4		14.8	77.9	45	6	AR088049	AR088049 Sequence
5		14.4	75.8	20	6	AR036920	AR036920 Sequence
6		14.4	75.8	20	6	AR097255	AR097255 Sequence
c 7		13.2	69.5	33	6	AR136084	AR136084 Sequence
8		13.2	69.5	40	6	I05997	I05997 Sequence 14
9		13.2	69.5	44	6	I08796	I08796 Sequence 18
c 10		13	68.4	25	6	AX116580	AX116580 Sequence
c 11		13	68.4	27	6	AR189327	AR189327 Sequence
c 12		12.8	67.4	25	6	AR154271	AR154271 Sequence
c 13		12.8	67.4	25	6	E38405	E38405 SC6 polypep
14		12.6	66.3	19	6	AX115503	AX115503 Sequence
15		12.6	66.3	43	6	AR152008	AR152008 Sequence
16		12.6	66.3	44	6	AR033897	AR033897 Sequence
17		12.6	66.3	44	6	AR175030	AR175030 Sequence
18		12.6	66.3	44	6	AX032462	AX032462 Sequence
19		12.6	66.3	48	6	E15948	E15948 Primer. 7/1
20		12.6	66.3	50	6	AX164813	AX164813 Sequence
c 21		12.4	65.3	18	6	A76055	A76055 Sequence 11
c 22		12.4	65.3	21	6	AX095087	AX095087 Sequence
23		12.4	65.3	31	6	AR090047	AR090047 Sequence
24		12.4	65.3	31	6	AR197082	AR197082 Sequence
25		12.4	65.3	31	6	I37209	I37209 Sequence 22
26		12.4	65.3	31	6	I37210	I37210 Sequence 22
27		12.4	65.3	31	6	I37211	I37211 Sequence 22
28		12.4	65.3	31	6	I94059	I94059 Sequence 22
29		12.4	65.3	31	6	I94060	I94060 Sequence 22
30		12.4	65.3	31	6	I94061	I94061 Sequence 22
31		12.4	65.3	40	6	A99027	A99027 Sequence 35
32		12.4	65.3	40	6	AR195344	AR195344 Sequence
33		12.4	65.3	45	9	HSBTIII60	Z73089 H.sapiens m
c 34		12.2	64.2	20	6	AX418798	AX418798 Sequence
35		12.2	64.2	21	6	A25404	A25404 CE gene mut
36		12.2	64.2	21	6	A25412	A25412 CE gene mut
c 37		12.2	64.2	31	6	AX249321	AX249321 Sequence
c 38		12.2	64.2	35	6	E36412	E36412 Protein rel
c 39		12.2	64.2	36	6	E16104	E16104 PCR primer
c 40		12.2	64.2	40	6	AX092544	AX092544 Sequence
c 41		12.2	64.2	45	6	AR032344	AR032344 Sequence
c 42		12.2	64.2	50	6	AX157400	AX157400 Sequence
43		12	63.2	20	6	AR130810	AR130810 Sequence
44		12	63.2	21	6	AR103495	AR103495 Sequence
c 45		12	63.2	21	6	AX096839	AX096839 Sequence

ALIGNMENTS

RESULT 1
AX008665
LOCUS AX008665 19 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 18 from Patent WO9966037.
ACCESSION AX008665
VERSION AX008665.1 GI:9996189
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Renzi,P.
TITLE Antisense oligonucleotides for treating or preventing atopic diseases and neoplastic cell proliferation
JOURNAL Patent: WO 9966037-A 18 23-DEC-1999;

```
           RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide inhibiting the CCR3 human
                     receptor"
BASE COUNT        2 a      6 c      6 g      5 t
ORIGIN

  Query Match             100.0%;  Score 19;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 7.8;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCTG 19
           ||||||||||||||||||||
Db       1 CTGGGCCATCAGTGCTCTG 19


RESULT 2
AX008666/c
LOCUS       AX008666                 19 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 19 from Patent WO9966037.
ACCESSION   AX008666
VERSION     AX008666.1  GI:9996190
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Renzi,P.
  TITLE     Antisense oligonucleotides for treating or preventing atopic
            diseases and neoplastic cell proliferation
  JOURNAL   Patent: WO 9966037-A 19 23-DEC-1999;
            RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Sense oligonucleotide for the CCR3 human receptor"
BASE COUNT        5 a      6 c      6 g      2 t
ORIGIN

  Query Match             100.0%;  Score 19;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 7.8;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCTG 19
           ||||||||||||||||||||
Db      19 CTGGGCCATCAGTGCTCTG 1


RESULT 3
AR088050/c
LOCUS       AR088050                 45 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 14 from patent US 5989834.
ACCESSION   AR088050
VERSION     AR088050.1  GI:10014813
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Gerald,C., Walker,M.W., Branchek,T. and Weinshank,R.L.
  TITLE     Uses of nucleic acid encoding neuropeptide Y/peptide YY (Y2)
            receptors nucleic acid encoding
  JOURNAL   Patent: US 5989834-A 14 23-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="unknown"
BASE COUNT       10 a     13 c     17 g      5 t
ORIGIN

  Query Match             83.2%;  Score 15.8;  DB 6;  Length 45;
  Best Local Similarity   89.5%;  Pred. No. 5.7e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCTG 19
           ||||| |||||||||| |||
Db      43 CTGGGGCATCAGTGCCCTG 25


RESULT 4
AR088049
LOCUS       AR088049                 45 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 13 from patent US 5989834.
ACCESSION   AR088049
VERSION     AR088049.1  GI:10014812
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Gerald,C., Walker,M.W., Branchek,T. and Weinshank,R.L.
  TITLE     Uses of nucleic acid encoding neuropeptide Y/peptide YY (Y2)
            receptors nucleic acid encoding
  JOURNAL   Patent: US 5989834-A 13 23-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="unknown"
BASE COUNT        7 a     12 c     12 g     14 t
ORIGIN

  Query Match             77.9%;  Score 14.8;  DB 6;  Length 45;
  Best Local Similarity   88.9%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCT 18
           ||||| |||||||||| ||
Db      28 CTGGGGCATCAGTGCCCT 45


RESULT 5
AR036920
LOCUS       AR036920                 20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 15 from patent US 5800997.
ACCESSION   AR036920
VERSION     AR036920.1  GI:5954776
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Beck,J.Joseph.
  TITLE     Detection of maize fungal pathogens using the polymerase chain
            reaction
  JOURNAL   Patent: US 5800997-A 15 01-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        3 a      5 c      6 g      6 t
ORIGIN

  Query Match             75.8%;  Score 14.4;  DB 6;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 GGCCATCAGTGCTCTG 19
           ||| ||||||||||||
Db       2 GGCAATCAGTGCTCTG 17


RESULT 6
AR097255
LOCUS       AR097255                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 15 from patent US 6071698.
```

```
ACCESSION   AR097255
VERSION     AR097255.1  GI:12805985
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Beck,J.Joseph.
  TITLE     DNA extraction buffer and method of use thereof
  JOURNAL   Patent: US 6071698-A 15 06-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT       3 a      5 c      6 g      6 t
ORIGIN

  Query Match           75.8%;  Score 14.4;  DB 6;  Length 20;
  Best Local Similarity  93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 GGCCATCAGTGCTCTG 19
          ||| ||||||||||||
Db      2 GGCAATCAGTGCTCTG 17


RESULT 7
AR136084/c
LOCUS       AR136084                  33 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 11 from patent US 6136580.
ACCESSION   AR136084
VERSION     AR136084.1  GI:14476756
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Fukuda,M. and Yeh,J.-C.
  TITLE     .beta.-1-6-N-acetylglucosaminyltransferase that forms core 2, core
            4 and I branches
  JOURNAL   Patent: US 6136580-A 11 24-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
BASE COUNT       8 a      8 c     10 g      7 t
ORIGIN

  Query Match           69.5%;  Score 13.2;  DB 6;  Length 33;
  Best Local Similarity  83.3%;  Pred. No. 1.8e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CTGGGCCATCAGTGCTCT 18
          |||| |||||  ||||||
Db     24 CTGGACCATCTCTGCTCT 7


RESULT 8
I05997
LOCUS       I05997                    40 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 14 from Patent EP 0275856.
ACCESSION   I05997
VERSION     I05997.1  GI:590816
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Bollen,A.J., Gheysen,D., Jacobs,P., Pierard,L. and Collen,D.J.
  TITLE     New plasminogen activators
  JOURNAL   Patent: EP 0275856-A1 14 27-JUL-1988;
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="unknown"
BASE COUNT       9 a      9 c     12 g      9 t      1 others
ORIGIN

  Query Match           69.5%;  Score 13.2;  DB 6;  Length 40;
  Best Local Similarity  83.3%;  Pred. No. 1.8e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 TGGGCCATCAGTGCTCTG 19
          ||| |||| | |||||||
Db     19 TGGTCCATGACTGCTCTG 36


RESULT 9
I08796
LOCUS       I08796                    44 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 18 from Patent WO 8804690.
ACCESSION   I08796
VERSION     I08796.1  GI:588501
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Bollen,A.J., Gheysen,D., Jacobs,P., Pierard,L. and Collen,D.J.
  JOURNAL   Patent: WO 8804690-A 18 30-JUN-1988;
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="unknown"
BASE COUNT      10 a     10 c     14 g     10 t
ORIGIN

  Query Match           69.5%;  Score 13.2;  DB 6;  Length 44;
  Best Local Similarity  83.3%;  Pred. No. 1.8e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 TGGGCCATCAGTGCTCTG 19
          ||| |||| | |||||||
Db     19 TGGTCCATGACTGCTCTG 36


RESULT 10
AX116580/c
LOCUS       AX116580                  25 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 1703 from Patent WO0129262.
ACCESSION   AX116580
VERSION     AX116580.1  GI:14033522
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 1703 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT       4 a      4 c     10 g      6 t      1 others
ORIGIN

  Query Match           68.4%;  Score 13;  DB 6;  Length 25;
  Best Local Similarity  86.7%;  Pred. No. 2.3e+04;
  Matches   13;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      5 GCCATCAGTGCTCTG 19
          |||:|||| ||||||
Db     19 GCCRTCAGAGCTCTG 5


RESULT 11
AR189327/c
```

```
LOCUS       AR189327                  27 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 4815 from patent US 6346398.
ACCESSION   AR189327
VERSION     AR189327.1  GI:20235292
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 4815 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT       10 a      5 c      7 g      4 t      1 others
ORIGIN

  Query Match             68.4%;  Score 13;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+04;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 CATCAGTGCTCTG 19
           |||||||||||||
Db      14 CATCAGTGCTCTG 2


RESULT 12
AR154271/c
LOCUS       AR154271                  25 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 4 from patent US 6238883.
ACCESSION   AR154271
VERSION     AR154271.1  GI:15122324
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Brown,A.M., Chapman,C.Gerald., Gloger,I.Simon., Evans,J.Rachel.,
            Cairns,W. and Herdon,H.Jonathan.
  TITLE     Neurotransmitter transporter SC6
  JOURNAL   Patent: US 6238883-A 4 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        5 a      8 c      7 g      5 t
ORIGIN

  Query Match             67.4%;  Score 12.8;  DB 6;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 3e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCT 16
           ||||||  ||||||||
Db      21 CTGGGCACTCAGTGCT 6


RESULT 13
E38405/c
LOCUS       E38405                    25 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  SC6 polypeptide and SC6 polynucleotide.
ACCESSION   E38405
VERSION     E38405.1  GI:18624976
KEYWORDS    JP 2000069981-A/3.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Brown,A.M., Chapman,K.J., Groga,I.S., Evans,J.R., Kern,W. and
            Hadon,H.
  TITLE     SC6 polypeptide and SC6 polynucleotide
  JOURNAL   Patent: JP 2000069981-A 3 07-MAR-2000;
            SMITHKLINE BEECHAM CORP PUBLIC LTD CO
COMMENT     OS   Artificial Sequence
            PN   JP 2000069981-A/3
            PD   07-MAR-2000
            PF   12-FEB-1999 JP 1999035070
            PR   28-AUG-1998 GB    9818890:7
            PI   ANTHONY M BROWN,KONRAD JERROLD CHAPMAN,ISRAEL SIMON GROGA, PI
             JOAN REYCHEL EVANS,WILLIAM KERN,HYU HADON
            PC   C12N15/09,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,
            PC   A61K39/00,
            PC   A61K45/00,A61K48/00,C07K14/47,C07K14/705,C07K16/28,C12N5/10,
            PC   C12P21/02,
            PC   C12Q1/68,G01N33/53,G01N33/566,G01N33/577//C12P21/08,C12N15/00,
            PC   C12N5/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .25
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        5 a      8 c      7 g      5 t
ORIGIN

  Query Match             67.4%;  Score 12.8;  DB 6;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 3e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCT 16
           ||||||  ||||||||
Db      21 CTGGGCACTCAGTGCT 6


RESULT 14
AX115503
LOCUS       AX115503                  19 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 626 from Patent WO0129262.
ACCESSION   AX115503
VERSION     AX115503.1  GI:14032445
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 626 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT        4 a      7 c      4 g      4 t
ORIGIN

  Query Match             66.3%;  Score 12.6;  DB 6;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCTG 19
           | | |||||||||| ||| |
Db       1 CAGAGCCATCAGTTCTCCG 19


RESULT 15
AR152008
LOCUS       AR152008                  43 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6232445.
ACCESSION   AR152008
VERSION     AR152008.1  GI:15118058
KEYWORDS    .
```

```
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Rhode,P.R., Acevedo,J., Burkhardt,M., Jiao,J.-a. and Wong,H.C.
  TITLE     Soluble MHC complexes and methods of use thereof
  JOURNAL   Patent: US 6232445-A 2 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="unknown"
BASE COUNT        7 a      21 c       9 g       6 t
ORIGIN

  Query Match             66.3%;  Score 12.6;  DB 6;  Length 43;
  Best Local Similarity   78.9%;  Pred. No. 4e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 CTGGGCCATCAGTGCTCTG 19
           | |||||| ||  ||||||
Db      13 CCGGGCCACCATGGCTCTG 31


Search completed: November 28, 2002, 18:20:40
Job time : 1105.97 secs
```